

SEQUENCE LISTING

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<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 METABOLIC PATHWAY PROTEINS

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 Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala
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 02130: Corynebacterium glutamicum

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 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
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 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
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 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
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 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
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 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
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 Val Ala Glu Val Ala His Arg Asn Ser Val Pro Leu Ile Ile Asp Asn
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 Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
 195 200 205
 Val Val Val Ala Ser Leu Thr Lys Phe Tyr Thr Gly Asn Gly Ser Gly
 210 215 220
 Leu Gly Gly Val Leu Ile Asp Gly Gly Lys Phe Asp Trp Thr Val Glu
 225 230 235 240
 Lys Asp Gly Lys Pro Val Phe Pro Tyr Phe Val Thr Pro Asp Ala Ala
 245 250 255
 Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu
 260 265 270
 Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala
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Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn
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Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser
325 330 335

Pro Asp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser
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Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe
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Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser Gln Ser Asp
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Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu
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420 425 430

Gly Phe Ala Ala Ile
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11200-

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 Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr Ser Lys Ala
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 Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe Ser Asn Glu
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 Val Leu
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Gly Ser Lys Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile
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Ile Val Pro Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val
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Thr Gly Arg Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys
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Glu Ile Glu Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys
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Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg
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Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr
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Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe
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Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr
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Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr
210 215 220

Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp
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Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val
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Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr
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Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val
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Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
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Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
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Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
 65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile
 85 90 95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
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Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
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Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
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Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
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Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
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Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
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Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
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Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
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Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
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Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
275 280 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
290 295 300

0010: "
0011: 948
0012: DNA
0013: Corynebacterium glutamicum

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0021: CD3
0022: 11.1.1.125
0023: EXA002.09

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Leu Thr Ile Pro Phe
1 5

ggc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag 163
Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
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gat acc ggc tta gat tta act cca gaa atg ggc gtc acc ctg tgt gac 211
Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
25 30 35

ggc acc gcc ggc atc ggt gct gat ggt atc ctc cgc ggc gtt aac gat 259
Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
40 45 50

gga cac gta gaa ggc tcc acc gtc gac cca tgc ctg tgt ttc atg gat 307
Ala Asp Val Gln Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
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Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val
70 75 80 85

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Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
90 95 100

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Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
105 110 115

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Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro
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 Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val
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 Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu
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acc cgc cca agc gcc atc atc gca ctc ggt gag gtg cag atc 925
 Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile
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taagattcgc gatgtagtt cgg 948

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(311): 275

(312): PBT

(313): *Corynebacterium glutamicum*

(400): 3

Leu Thr Ile Pro Phe Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile
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Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val
 20 25 30

Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu
 35 40 45

Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser
 50 55 60

Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met
 65 70 75 80

Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly
 85 90 95

Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg
 100 105 110

His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val
 115 120 125
 Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn
 130 135 140
 Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu
 145 150 155 160
 Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu
 165 170 175
 Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn
 180 185 190
 Val Glu Ile Val Thr Gln Leu Glu Asp Asp Ala Val Ser Met Arg Val
 195 200 205
 Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val
 210 215 220
 Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
 225 230 235 240
 Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp
 245 250 255
 Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu
 260 265 270
 Val Gln Ile
 275

CL10 - 9
 CL11 - 1491
 CL12 - DNA
 CL13 - Corynebacterium glutamicum

CL14
 CL11 - CDS
 CL12 - (101)..(1463)
 CL13 - EXS02970

CL10 - 9
 aacgcgaaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60
 ttttttaag atttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tat gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aca gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259

His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
4 45 50

gac gaa ggt tcc acg ctg tac gac ttc gac ggc aac ggc ttc atc gac 307
Ala Gln Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tgg gaa aac tta ggc cac aac aac cct cga 315
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta ggt gag ggc atc cag cgc cca gca gac cgg ttg aac aac atc aac 403
Leu Val Gln Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

cag gac ttc ggt aat gat ggg cgc tct gat ggt ggt gaa aag atc gtc 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tgg atg ggc cgt ggc gaa ttc ttc cac ggg ttt ttc aac aac ggt ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gac gac ggc atc gag cac tcc atc cgc atg gat cgc ctg cac aat gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac gaa atc ctg tcc gaa ttc cgc agc tac cac ggc gca aat gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc ggc atg atg ctg acc ggc gaa cac cgc cgc ctg ggc aac cgc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
170 175 180

acc gac cca gat atc tac cac ttc tgg gaa cca ttc ctg cac cgt tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
185 190 195

tca ttc ttt ggc acc acc caa gaa gaa gaa tcc gaa cgc cca ctg aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
200 205 210

cac ttg gaa gat gtc atc cgc ttt gaa ggt gat ggc atg atc gaa ggc 787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
215 220 225

atc gtc ctg gag cca gtc gtc gga tca tca gga atc atc ctg cca cca 835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230 235 240 245

gca ggt tac tta aat ggc gtc ggc gaa ttt tgc aac aag cac gtc atc 883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
250 255 260

ctc ttc atc ggc gac gaa gtc atg gtc gga ttc gga ggc acc gaa aaa 931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
265 270 275

ctg ttt gat tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile

280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctg ggt ggc atc 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

ctg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctg acc tac tcc gga cgc cca ctt gca gta gca ccc gcc aag 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcc ctg gag att tac gcc gaa gga gag atc att cca cgc gta gct 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

gga gtt gcc act gaa ctg atc gaa cct cgc ctt cgt gaa cta gcc gaa 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta acc atc gct gat gtg cgg gcc atc gga ttc ttc tgg gca 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

ctg gaa ttc aat gca cgc gcc act gcc atg gct gcc cgt gct gca gaa 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc gcc gtg tgg ccg atg atc tcc ggt aac cga ttc cgc 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420

atc ccg ccg ccg ctg acc acc act gat gac gaa ctg gta gca ctg ctg 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435

gac ccg ctg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450

ccg ctg ttc taagttttct agataacaag gcc 1491
 Ala Leu Phe
 455

4100-10

4211-456

412- PFT

4213- Corynebacterium glutamicum

4100-10

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Asn
 165 170
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 175 180 185 190
 Phe Leu His Ile Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe
450 455

210 11

211 1330

212 DNA

213 Corynebacterium glutamicum

220

221 CDS

222 (121)...(134)

223 FRXA01039

400 11

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aaataaaa acatataaat attctgggga gtagaactggt tta gca ttg aag ggt 116
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc ggc cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc ggc cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tgg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag ggc atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

cag gcc ttc ggc aat gat gtg cgc ttc gat gtt gct gca aag atc gtg 451

Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val	Ala	Ala	Lys	Ile	Val		
			105					110					115				
tcg	atg	gac	cgt	ggc	gaa	ttc	tcg	caa	gtg	ttt	ttc	acc	aac	ggc	ggc	499	
Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe	Phe	Thr	Asn	Gly	Gly		
		120					125					130					
gac	gac	gac	atc	gag	cac	tcg	atc	cgc	atg	ggt	cgc	atg	gac	acc	gga	547	
Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala	Arg	Leu	His	Thr	Gly		
	135					140					145						
cgc	aac	aaa	att	ctg	tcg	gca	tac	cgc	agc	tac	caa	ggc	gca	acc	gga	595	
Arg	Asn	Lys	Ile	Leu	Ser	Ala	Tyr	Arg	Ser	Tyr	His	Gly	Ala	Thr	Gly		
150				155				160				165					
tcg	ggg	arg	atg	ctc	acc	ggc	gaa	caa	cgc	cgc	ctg	ggc	aac	ccc	acc	643	
Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg	Leu	Gly	Asn	Pro	Thr		
				170				175						18			
acc	gac	caa	gat	atc	tac	caa	ttc	tgc	gca	caa	ttc	atg	gac	caa	tcg	691	
Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
		185						190				195					
tcg	ttc	tac	gac	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	ggc	gca	ctc	atg	739	
Ser	Phe	Phe	Ala	Thr	Thr	Glu	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
	200					205					210						
caa	atg	gaa	gat	gtc	atc	ggc	ttc	gaa	ggt	ggt	ggc	atg	atc	gaa	gag	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
	15				220					22							
atc	acc	ctg	gag	cca	ggg	gla	gaa	cca	caa	gaa	atc	atc	ctg	caa	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230				235						240				245			
gaa	gtt	tac	tta	aat	cgc	gtg	ccc	gaa	ctt	tcg	aat	cag	caa	ggt	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250				255						260			
ctc	ttc	atc	gac	gac	gaa	gtc	atg	gtt	gga	ttc	gga	ggc	acc	ggc	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
		265					270						275				
ctg	ttc	gat	tac	caa	cat	gat	ggc	gac	gat	ttc	cag	cca	gac	atc	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Glu	Pro	Asp	Met	Ile		
		280					285					290					
acc	ttc	gac	aag	cgt	gtt	aac	gca	ggc	tac	ggc	cca	ctc	ggc	ggc	atc	1027	
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile		
	295					300					305						
gtt	atg	acc	caa	tca	atc	cgc	gat	acc	ttc	gga	tca	gag	gca	tac	tcg	1075	
Val	Met	Thr	Glu	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
310					315					320				325			
ggc	gga	ctc	acc	tac	tcg	gga	caa	cca	ctt	gca	gta	gca	ccc	ggc	aag	1123	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
			330					335						340			
gca	gca	ctg	gag	att	tac	ggc	gaa	gga	gag	atc	att	cca	cgc	gta	ggt	1171	
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala		

345	350	355	
aga ctt ggc ggt gaa ctg atc gaa cct cgc ctt cgt gaa cta ggc gaa			1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			
360	365	370	
gaa aac gta ggc atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca			1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala			
375	380	385	
gtg gag ttc aat gca gac gcc act ggc atg gct gcc ggt gct gca gaa			1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu			
390	395	400	405
ttc aag gaa cgc ggc			1330
Phe Lys Glu Arg Gly			
410			

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Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro	
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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly	
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Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly	
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His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg	
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Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val	
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Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe	
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Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala	
130	140
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr	
145	155
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg	
165	175
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro	
180	190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Glu Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
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 (112): INA
 (113): Corynebacterium glutamicum

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 (116): (101)..(769)
 (117): EXC02390

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 Val Glu Trp Thr Ala
 1 5
 ttt ggc acc ctg att ctg ctg aat ttg gtc ggc agt tta tcc ccg ggg 163

Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
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 cct gat acc ttt ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc ttc 211
 Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
 25 30 35
 ggg atc gct ggg gtc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc ggc 259
 Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
 40 45 50
 acg ctg acg gta gtc gga gga ggc ggc ggc ggc ggc ggc ggc ggc ggc 307
 Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
 55 60 65
 att ctg gga atc atc atc atc atc atc atc atc atc atc atc atc atc 355
 Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
 70 75 80
 ggg tac aag ttc ctg cgc tgc ggc ggc ggc ggc ggc ggc ggc ggc ggc 403
 Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Gly Leu Ile Asp Ala Arg
 90 95 100
 gag ttc cgt ttc aac ggc gat ggc ggc ggc ggc ggc ggc ggc ggc ggc 451
 Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Gln
 105 110 115
 gga ctg gga acc cgc act gag gta tat cca cca cca ggt ttg ggc acc aac 499
 Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
 120 125 130
 ctg tca aac cgt aac gtt ttc atg tac ttc ggc ggc atc ctg gct cca 547
 Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
 135 140 145
 tgg atg cca ggc ccc cca tca ccc gta ctg ggc ttc ttc atc atc gta 595
 Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
 150 155 160 165
 gag atc tta gtc gag acc ttt gtt acc ttc ttc gct gtc tgc ctg att 643
 Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
 170 175 180
 gtc ttc acc gag cgt gtc cgc aaa ggc atg ctg cgt gca ggt ccc tgg 691
 Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
 185 190 195
 ttt gac ctg ctt gct ggc att gtc ttc ttc gtt gtc ggt gtc act ctg 739
 Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
 200 205 210
 ctg tat gaa ggc ctg acc ggt tta ctg ggc taaaggcata aaaaatgggt 789
 Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
 215 220
 tcc 792

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<215> Corynebacterium glutamicum

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Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
35 40 45

Ile Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
50 55 60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
65 70 75 80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Gln
85 90 95

Ile Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
100 105 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
115 120 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
130 135 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
145 150 155 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
165 170 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
180 185 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
195 200 205

Val Gly Val Thr Leu Leu Tyr Gln Gly Leu Thr Gly Leu Leu Gly
210 215 220

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Leu Leu Leu Gly Gly

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aac cct gcc gag atc gac cag gtt tta ggt gcc gat caa acc cag atc			163
Asn. Pro Ala Glu Ile Asp Glu Val Leu Gly Gly Asp Gln Thr Gln Ile			
	10	20	
gag tct gga gag tcc acc gga gcc gcc gag ttt gat cac tcc caa acc			211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr			
	25	35	
ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tcc acc tca			259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser			
	40	50	
ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt			307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly			
	55	65	
atc gaa tac acc gag cag aca ttg act ctt ttc aaa aac ttc acc caa			355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln			
	70	80	85
acc gcc tgc ggt ttc ggt tct gcc tcc act ggg cag ttt ttc tgt ccg			403
Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro			
	90	95	100
tca gac caa gat gct tat ttg gac ctg act ttc ttc gat cag atg cgt			451
Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg			
	105	110	115
cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcc			499
Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala			
	120	125	130
cac gag tac gcc cac cac gtc caa aac ctg gag ggc aca ctg gga ctg			547
His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu			
	135	140	145
tcc aat tac aac gat ccg gcc gct gat tcc aac gcc gtc aag atc gag			595
Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu			
	150	155	160
ttg cag gcc gat tgc tac gca gcc att tgg gct aat cac tcc acc gaa			643
Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu			
	170	175	180
ggc ccg gat ccg cta ctg caa ccc atc acc gaa tct gag cta gat tcc			691
Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser			
	185	190	195
gct ttc ctt gct gca agc gcc gtc gcc gag gac aat atc cag caa cga			739
Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg			
	200	205	210
tcc ggt gcc gat gtc aat cct gaa agc tgg act cac gcc tca tgg cag			787
Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln			
	215	220	225
cag cgc aaa cag gcc ttc ctg gcc gcc tac aac acc gcc cag atg agc			835
Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser			
	230	235	240
			245

gac tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg 884
 Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
 250 255

cttttgcagc tct 897

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 <212> FRT
 <213> Corynebacterium glutamicum

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 20 25 30
 Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
 35 40 45
 Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
 50 55 60
 Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65 70 75 80
 Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
 85 90 95
 Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
 100 105 110
 Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
 115 120 125
 Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
 130 135 140
 Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
 145 150 155 160
 Ala Val Lys Ile Gln Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
 165 170 175
 Asn His Ser Ser Gln Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
 180 185 190
 Ser Gln Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
 195 200 205
 Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
 210 215 220
 His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
 225 230 235 240
 Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
 245 250 255

Asp Ala

(210> 17
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(212> DNA
(213> Corynebacterium glutamicum

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(222> (101)..(748)
(223> RXC01207

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aattttaaac aatcggtaga ccaacttaag gagaaaaaca gtg agc aga atc tat 115
Val Ser Arg Ile Tyr
1 5
gac tgt gcc gac caa gac tcc cgt gca gca gcc cta aag gcg ggt gtc 163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
10 15 20
tac gca gta aaa att ggt cag tta gcc gta ttc ccc aag gat acc att 211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
25 30 35
tat gga ttc gcc tgc gac ggt ttc aac aac aag gca gta gcc aac att 259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
40 45 50
ctg gcc acc aaa cac cgt gcc ccc gat atg ccc gtt cca gtg ctg gtc 307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
55 60 65
ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcc cag 355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
70 75 80 85
gca aaa gcc ctt gtg gag gcc ttc tgg cct ggt gga ctg tcc atc atc 403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
90 95 100
gtt ccg cag gca cca agc ctt ccg tgg aac ctt gcc gat acc cgt gcc 451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
105 110 115
acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg 499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
120 125 130
ggc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat 547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
135 140 145
act cct cca acc acc gtg ctg gag gct cgt cag cag ctg aac caa aat 595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Glr Asn
150 155 160 165

gtc ggt gtc tac ctc gat ggt ggt gaa tgc gag ctg gcc acc cat tca 643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
170 175 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt 691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
185 190 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtc tcc gaa gaa 739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
200 205 210

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Ser Leu Arg
215

<210> 18
<211> 216
<212> FRT
<213> Corynebacterium glutamicum

<400> 18
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20 25 30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
35 40 45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
50 55 60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
65 70 75 80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
85 90 95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
100 105 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
115 120 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
130 135 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
145 150 155 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
165 170 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
180 185 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu

195

200

205

Gly Val Ser Ala Glu Ser Leu Arg
210 215

<210> 19

<211> 1020

<212> INA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1003)

<223> EXC 0657

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tyaacgga; gattcaccbaa tcaatgaag gtcgacogac atg agc act gaa gac 115
Met Ser Thr Glu Asp
1 5

att ttc gtc gta gca gta gat ggc tcg gac gcc tca aac caa gct gtt 163
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
10 15 20

ggt tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg 211
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
25 30 35

gct tcc agc tac acc atg cct aac ttc ctc tac gca gag gga atg gtt 259
Ala Ser Ser Tyr Thr Met Pro His Phe Leu Tyr Ala Gln Gly Met Val
40 45 50

cca cca cca gag ctt ttc gat gat ctc cag gcc gaa gcc ctg gaa aag 307
Pro Pro Gln Gln Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
55 60 65

att aac gaa gcc cct gac ttc ggc cat gag gta ggc cca gaa atc aag 355
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys
70 75 80 85

atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa 403
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
90 95 100

atg tcc ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc 451
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly
105 110 115

gga ctc tcc gga atg gtc atg gcc tcc gtc tcc ggt gca gtg gtc agc 499
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser
120 125 130

cac gaa aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac 547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
135 140 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa 595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu

150 155 160 165

gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt 643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg
170 175 180

ggc ggc gaa ctc gtt gca gtt ctc acc tgg atg gac atg cag gta cag 691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
185 190 195

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
200 205 210

gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg 787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val
215 220 225

gaa aag tac cca act gta acc gtc aag aag atc atc acc cgt gac cgc 835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
230 235 240 245

cca ctt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
250 255 260

ctt cgt tcc cat gct cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
265 270 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
280 285 290

cgc cca cct gag aag att sag aag tagttttcttt taagtttcga tgc 1026
Arg Pro Pro Glu Lys Ile Lys Lys
295 300

210-20
211-301
212-PET
213-Corynebacterium glutamicum

400-20
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
1 5 10 15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
20 25 30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
35 40 45

Ala His Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
50 55 60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile

85

90

95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
 100 105 110
 Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
 115 120 125
 Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
 130 135 140
 Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
 145 150 155 160
 Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
 165 170 175
 Glu Ala Gln Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
 180 185 190
 Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
 195 200 205
 Gln Trp Asp Glu Val Gln Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
 210 215 220
 Leu Ala Pro Leu Val Gln Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
 225 230 235 240
 Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Gln Ala Ser Glu Asn
 245 250 255
 Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
 260 265 270
 Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
 275 280 285
 Ser Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
 290 295 300

110 - 21
 111 - 1052
 112 - DNA
 113 - Corynebacterium glutamicum

1140 -
 1151 - CDS
 1152 - (101) .. (1036)
 1153 - FK000552

1400 - 21
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 Val Ala Thr Ser Lys
 1
 5
 att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa ggg gtt 163
 Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val

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cag ctg tgg cag cgt gag ctg tgc gag tca ctg aat ctt cgt ggt cgc			211
Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg			
25	30	35	
atc ctg atc tcc act cdc ggc atc aat gta acc ggc ggc gga gat att			259
Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile			
40	45	50	
gat gat tgc aag ggc ttc att aaa aag acc cgc gag cac cca ggt ttc			307
Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe			
55	60	65	
aac cgc atg cag ttc aag tgg tcc gag ggt ggc ggt gag gat ttc cca			355
Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Pro Pro			
70	75	80	
cag ctg act gta aaa gta ctc gat gag atc gta gcc ttc ggc gat cca			403
Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro			
90	95	100	
gat gag ttc aaa ggc gat gta aac ggc gta gta ggt ggc ggc ggt cca			451
Asp Glu Leu Lys Val Asp Gln Asn Gly Val Val Gly Gly Gly Val His			
105	110	115	
ctc aaa cca cag cag gta aac gag ctg gta gaa gcc cgt ggc gat gaa			499
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu			
120	125	130	
gtt ggc ttc ttc aac ggt ctc aac ggc atg gaa gcc cag atc gat aag			547
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys			
135	140	145	
ctc aag aac ggt ggt gta ctc gta gta gaa acc act cat gat ttc aac			595
Phe Lys Asp Ala Val Val Pro Asp Val Gln Thr Thr His Asp Pro Ile			
150	155	160	
gca gaa att gag tct gaa aaa tcc gac gat ctg aaa gac aag cct gtc			643
Ala Glu Ile Gln Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val			
170	175	180	
gtc acc tcc tcc acc ggc gta att cgt cct gag atc ctg agt tcc ctg			691
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu			
185	190	195	
atg atc aac cct ggt ttc aaa gag gtc tcc cca atc gat ggc ggc atc			739
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile			
200	205	210	
gtt cgc tcc gcc gag cag ttc ggc aac aag ggc ctg tgg gaa ggt tcc			787
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser			
215	220	225	
ctc tcc gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tcc			835
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr			
230	235	240	
aaa gag ctg ggc ccc tcc atc cat tgc gat act ccc acc aac aaa ttc			883
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe			
250	255	260	

gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc qtg ttg atg tgc 931
 Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
 265 270 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc 979
 Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
 280 285 290

tgt gca gca att gct ggc gat ttc gct gag gaa gga att gat cgc ctc 1027
 Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
 295 300 305

ggt act tct taaaaagggt atggtggctg ggt 1059
 Val Thr Ser
 310

Q210: 12

Q211: 31:

Q212: PRT

Q213: Corynebacterium glutamicum

Q400: 12

Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
 1 5 10 15

Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
 20 25 30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
 35 40 45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
 50 55 60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65 70 75 80

Ala Gln Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
 85 90 95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Gln Asn Gly Val Val
 100 105 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
 115 120 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
 130 135 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Gln Thr
 145 150 155 160

Thr His Asp Phe Ile Ala Glu Ile Gln Ser Gly Lys Tyr Asp Asp Leu
 165 170 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
 180 185 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln

195	200	205
Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly 210	215	220
Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu 225	230	235 240
Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr 245	250	255
Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu 260	265	270
Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His 275	280	285
Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln 290	295	300
Gly Ile Asp Pro Leu Val Thr Ser 305	310	
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<223> RXA00034		
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gggggtaact gtcaggaact agatcgaaaag gtgcacaaag gtg gcc ctg gtc gta 115		
	Val Ala Leu Val Val	1 5
cag aaa tat gcc ggt tcc tcc att gag agt gcc gaa cgc att aga aac 163		
Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn	10 15 20	
gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg 211		
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val	25 30 35	
gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt 259		
Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu	40 45 50	
gca gcc gca gtg aat ccc gtt ccc cca gct cgt gaa atg gat atg ctc 307		
Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu	55 60 65	
ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att 355		
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile	70 75 80 85	

gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt 402
 Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly
 90 95 100

gta ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act 451
 Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr
 105 110 115

cca ggt cgt gta cgt gaa gca ctc gat gag ggc aag atc tcc att gtt 499
 Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val
 120 125 130

gat ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg 547
 Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu
 135 140 145

ggt ctt ggt ggt tct cag acc act gca gtt ggc ttg gaa ggt ggt ttg 595
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Leu Ala Ala Ala Leu
 150 155 160 165

aac gac gat gta tgt cag att tac tgc gac gtt gac ggt gta tat acc 643
 Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val Asp Gly Val Tyr Thr
 170 175 180

gcc gac cag cgc atc ctt cct aat gca cag aag ctg gaa aag ctc acc 691
 Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys Leu Glu Lys Leu Ser
 185 190 195

ttc gaa gaa atg ctg gaa ctt ggt ggt gtt ggc tcc aag att ttg ctg 739
 Ile Glu Glu Met Leu Glu Leu Ala Ala Val Gly Ser Lys Ile Leu Val
 200 205 210

ctg cgc agt ctt gaa cac ggt cgt gca ttc aat gag cca ctt cgc gta 787
 Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn Val Pro Leu Arg Val
 215 220 225

cgc tgc tct tat agt act gat ccc cgc act ttg act gcc ggc tct arg 835
 Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu Ile Ala Gly Ser Met
 230 235 240 245

gag gat att ctt gta gaa gaa gca gtc ctt acc ggt gtc gca acc gac 883
 Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp
 250 255 260

arg tcc gaa gcc aaa gta acc gtt ctg ggt att ttc gat aag cca ggc 931
 Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly
 265 270 275

gag ctt gag aag gtt ttc cgt ggc ttg ggt gat gca gaa atc aac att 979
 Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile
 280 285 290

gac atg gtt cag cag aac gtc tct tct gta gaa gac ggc acc acc gac 1027
 Asp Met Val Leu Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp
 295 300 305

atc acc ttc acc tgc cct cgt tcc gac ggc cgc cgc gcg atg gag atc 1075
 Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg Arg Ala Met Glu Ile
 310 315 320 325

ttg aag aag ctt cag gtt cag ggc aac tgg acc aat gta ctt tac gac 1123

Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp
 330 335 340

gag cag gtc ggc aaa gtc tcc ctg gtc ggt gct ggc atg aag tct cae 1171
 Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His
 345 350 355

cca ggt gtt acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg 1219
 Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val
 360 365 370

aac atc gaa ttc att tcc acc tct gag att cgt att tcc gtc ctg atc 1267
 Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
 375 380 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc 1315
 Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
 390 395 400 405

cag ttc gac ggc gaa gac gaa gac gtc gtc tat gca ggc acc aga cgc 1363
 Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
 410 415 420

taagattta aagagtagt ttt 1386

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 <213> Corynebacterium glutamicum

<400> 24
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 20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
 35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
 50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
 85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
 100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
 115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
 130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
 145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
 165 170 175
 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
 180 185 190
 Leu Gln Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
 195 200 205
 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
 210 215 220
 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
 225 230 235 240
 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
 245 250 255
 Gly Val Ala Phe Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
 260 265 270
 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
 275 280 285
 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
 290 295 300
 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
 305 310 315 320
 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Glu Gly Asn Thr Thr
 325 330 335
 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
 340 345 350
 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
 355 360 365
 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
 370 375 380
 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
 385 390 395 400
 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
 405 410 415
 Ala Gly Thr Gly Arg
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(210) 15
 (211) 115a
 (212) DNA
 (213) *Corynebacterium glutamicum*

(216)
 (217) CDS
 (222) (101)..(1132)

4223 PXA-0533

4400- 25

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Met Thr Thr Ile Ala
1 5

att act gat gca acc ggc cag gtc ggc cag gtt atg cgc acc ctt ttg 163
Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu
10 15 20

aaa cag cgc aat ttc cca gct gac act ggt cgt ttc ttt gct tcc cca 211
Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro
25 30 35

cgt tcc gaa gcc cgt aag att gaa ttc cgt ggc acc gaa atc gag gta 259
Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val
40 50

aaa cag att act cag gca acc gag gag tcc ctc tag gac atc gac ggt 307
Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu Lys Asp Ile Asp Val
55 60 65

cgt ttc ttc tcc gct gga ggc acc gct tcc aag tag tcc gct cca ctg 355
Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys Gln Tyr Ala Pro Leu
70 75 80 85

ttc act gat gca ggc ggc acc ggt ggc gat acc cct tct gct tgg cgc 403
Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn Ser Ser Ala Trp Arg
90 95 100

arg tcc gat gag gct cca cca atc gtc tcc gag ggc aac cct tcc gac 451
Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu Val Asn Pro Ser Asp
105 110 115

cag gat tcc ctg gtc aag ggc att att ggc aac cct aac tgc acc acc 499
Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn Pro Asn Cys Thr Thr
120 125 130

atg gct gat atg cca ggt ctc aag cca ctt cag gat gca gct ggt ctt 547
Met Ala Ala Met Pro Val Leu Lys Pro Leu His Asp Ala Ala Gly Leu
135 140 145

gta aac ctc cag gtt tcc tct cag cag gct gtt tcc ggt tct ggt ctt 595
Val Lys Leu His Val Ser Ser Tyr Gln Ala Val Ser Gly Ser Gly Leu
150 155 160 165

gca ggt gat gaa acc ctg gca aag cag gtt gct gca gtt gga gac cac 643
Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala Ala Val Gly Asp His
170 175 180

aac gtt gag ttc gtc cat gat gga cag gct gct gac gca ggc gat gtc 691
Asn Val Glu Phe Val His Asp Gly Gln Ala Ala Asp Ala Gly Asp Val
185 190 195

gga cct tat gtt tca cca atc gct tac aac gtc ctg cca ttc gcc gga 739
Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val Leu Pro Phe Ala Gly
200 205 210

aac ctc gtc gat gac ggc acc ttc gaa acc gat gaa gag cag aag ctg 757
 Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp Glu Glu Gln Lys Leu
 215 220 225

 agc aac gaa tcc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835
 Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser
 230 235 240 245

 ggc acc tgc gtc cgc gtg cgg gtt ttc acc ggt cag aag ctg acc att 883
 Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
 250 255 260

 cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931
 His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
 265 270 275

 ttg agt gcc gct tca ggc gtc aag att gtc gac gtc cca acc cca gtt 979
 Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
 280 285 290

 gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc ggt cag gac 1027
 Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
 295 300 305

 tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac 1075
 Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
 310 315 320 325

 aac ctc cgc aag ggt gct gag gta aac acc atc cag atc gct gag ctg 1123
 Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu
 330 335 340

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 Leu Val Lys

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 <213> Corynebacterium glutamicum

<400> 26
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 20 25 30

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 35 40 45

 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
 50 55 60

 Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
 65 70 75 80

 Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
 85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
100 105 110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp
275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
325 330 335

Gln Ile Ala Glu Leu Leu Val Lys
340

4116-27

4116-508

4116-DNA

4116-Corynebacterium glutamicum

4216

4216-CHS

4216-(69)...(608)

4216-EXA0284

4400-27

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tggacgtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
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acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
15 20 25 30

cac tcc ggg ctg aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
35 40 45

acc ggc aaa atc gtg acg aca act atc gac acc gac gca gcc ctc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
50 55 60

gac aac tac tat gaa tgg ctg ctc ctt ttc ctc ttc tac cag ctc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
65 70 75

ctc agc ctc cag aac atc aac cta gac ggc att ttc gac ctg atc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
80 85 90

atg gtc gta tgg acc aac ttc gga cag ttc gca ttc gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
95 100 105 110

ctc acc ctc ggg cgc ctg taa cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcc ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
130 135 140

ggc atc ggt gac gcc gac cgc gtc cga ctt ggc cgc tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
160 165 170

ctc ggc gct tcc atg gtt 608
Leu Gly Ala Ser Met Val
175 180

<210> 28

<211> 180

<212> PRT

<213> Corynebacterium glutamicum

<400> 28

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
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20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
 35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
 50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
 65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
 85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
 100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
 115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
 130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
 145 150 155 160

Thr Val Met His Val Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
 165 170 175

Ala Ser Met Val
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1207)
 <223> RXA02022

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 Val Asn Ser Glu Leu
 1 5

aaa cca gga tta gat ctc ctc ggc gac cca att gtc att act caa cgt 163
 Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
 10 15 20

ttg gta gat ata cgg agt cgg tgg ggt cag gaa aag cag att got gat 211
 Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
 25 30 35

gaa att gaa gat gac att cgg aac att aat cta att ggt gta gag gtc 259
 Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
 40 45 50

ttc cgc ttc aac aac aac gtt ctt ggt cgc acg aac agg gga ttg gcc	307
Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala	
55 60 65	
tcg agg gtc atg ctt ggt ggt cat atc gat aca gtg cgg atc ggg gac	355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp	
70 75 80 85	
aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt gcc acc	403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr	
90 95 100	
gtc gat atg aaa tct ggg ttg ggg gtg tat ttg cat aat ttt gcc acc	451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr	
105 110 115	
ttg gcc acg tgg acg gag ctt aaa cat gat ttg acg ctg att gag tat	499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr	
120 125 130	
aat ttc gat gaa gtt ggt gat aac ctt aat tgt ttg ggt aac att gtt	547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg	
135 140 145	
gat gag cat ctg gat tgg ttg ggg ggt gat ttg ggg ttg ctg ggt gag	595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu	
150 155 160	
cct act ggc gcc tgg att gat ggg ggc tgc cag gcc aat ctt cgc atc	643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Glu Gly Asn Leu Arg Ile	
170 175 180	
aag gtg acg ggg cat ggt gtg cgt gcc cat tgg ggg aga aat tgg ttg	691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu	
185 190 195	
ggt gat aat ggg atg cat aag ttg tgg cgg atc att tgg aag gtt ggt	739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala	
200 205 210	
ggc tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa	787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu	
215 220 225	
ggc ctc aac atc gtt ttc tgc gaa tgg ggc gtg gca aac aac gtc att	835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile	
230 235 240 245	
cca gac ctc ggg tgg atg aac ctc aac ttc cgt ttc ggg cgg aat cgc	883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg	
250 255 260	
gat ctc aac gag ggg atc gag cat gtc gtc gaa acg ctt gag ctt gac	931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp	
265 270 275	
ggt caa gac gcc att gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc	979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala	
280 285 290	
ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc	1027

Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val
295 300 305

ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt 1075
Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
310 315 320 325

ttt tca gcc atg gga att cca gcc cta aac ttt ggc tct ggt gat cca 1123
Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
330 335 340

agt ttc ggc cat aaa cgc gac gag cag tgc cca gtc aag caa atc aag 1171
Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
345 350 355

gat gtc gca gca att ttg aag cag ttc ctg agc gag taacgatt 1217
Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
360 365

gggggttattc atg 1230

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<211> 369

<212> CRT

<213> Corynebacterium glutamicum

<100> 30

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Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu
20 25 30

Lys Glu Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
35 40 45

Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
50 55 60

Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
65 70 75 80

Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
85 90 95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
100 105 110

His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
115 120 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
130 135 140

Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
145 150 155 160

Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
165 170 175

Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
 180 185 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile
 195 200 205

Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly
 210 215 220

Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val
 225 230 235 240

Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg
 245 250 255

Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu
 260 265 270

Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp
 275 280 285

Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly
 290 295 300

Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp
 305 310 315 320

Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe
 325 330 335

Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro
 340 345 350

Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser
 355 360 365

Glu

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> EXA00044

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 Met Ala Ser Ala Thr
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ttc acc ggc gtg atc cca ccc gta atg acc cca atc cag gcc gac gcc 163
 Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
 10 15 20

agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat	211
Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn	
25 30 35	
ggt ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gcg gca	259
Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala	
40 45 50	
ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag	307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu	
55 60 65	
cac acc gca ggc cgc ggt ccc gca act gct ggt gtc att gaa acc acc	355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr	
70 75 80 85	
act gat ggc gtc att gag ctc ggc gaa gat gat ctc gag gtc ggt gcc	403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala	
90 95 100	
gaa gtc att gtc ggt act gca act ttc cac acc cgc acc ctc gat gtc	451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val	
105 110 115	
gaa atc gat gaa cac ttc cgc aag atc cac gtc gtc ttc cca gag ctt	499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu	
120 125 130	
cca atg ttc ggc tac aac atc cca gtc tgc gtc cac ttc aac ttc aac	547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn	
135 140 145	
tca gtc atc att ttg aag ctc gcc aag gat gga gtc ctt gca tgc aac	595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr	
150 155 160 165	
aag gat ttc agt ggc aat gat ggc gca atc cgc tca ctg atc gaa gct	643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala	
170 175 180	
cgt gat gat ggt gga ctc act gag cag ttc aag atc ctc acc ggc agc	691
Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser	
185 190 195	
gaa acc acc gtt gat ttc gcc tac ctt ggc ggt gcc gat gga gtt gtc	739
Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val	
200 205 210	
cca ggc ctg ggc aat gtt gat cct gca gca tac gca gct tta gca aaa	787
Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys	
215 220 225	
ctc tgc ctc gat gga aag tgc gca gaa gct gct gct ttg cag aag cgc	835
Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg	
230 235 240 245	
atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg	883
Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met	
250 255 260	
tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac	931

Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His
 265 270 275
 ctt ggc att att gaa tcc aat ggc atg gca gtt cct cac cag agc etc 979
 Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
 280 285 290
 agc gac gaa gaa act gct ggc att cac ggc att gtt gat gaa ttc atg 1027
 Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
 295 300 305
 tac acc gct taaggccac acctcatgac tga 1059
 Tyr thr Ala
 310

<210> 32

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro
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 Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
 35 40 45
 Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
 50 55 60
 Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
 65 70 75 80
 Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
 85 90 95
 Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
 100 105 110
 Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
 115 120 125
 Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
 130 135 140
 His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
 145 150 155 160
 Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
 165 170 175
 Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
 180 185 190
 Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
 195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala
225 230 235 240

Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly
245 250 255

Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys
260 265 270

Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val
275 280 285

Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile
290 295 300

Val Asp Glu Phe Leu Tyr Thr Ala
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)...(344)

<223> RXA00823

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Met Gly Ile Lys Val
1 5

ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala
10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp
25 30 35

gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp
40 45 50

ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn
55 60 65

aac ggc att tct ggc gtt gtt gga acc acg ggc ttc gat gat gct cgt 355
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg
70 75 80 85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val

90	95	100	
ctg atc gca cct aac ttt gct atc tct ggc gtc ttg acc atg gtc ttt			451
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe			
105	110	115	
taa aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att cag ctg			499
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu			
120	125	130	
cac cac ccc aac aag ctg gat gca cct tca ggc acc ggc atc cac aet			547
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr			
135	140	145	
gat cag agc att gct ggc gca cgc aaa gaa gca ggc atg gac gca cag			595
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln			
150	155	160	165
gaa gaa gag acg gag cag gca cct gag ggt ttc cgt ggc gca ggc gta			643
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val			
170	175	180	
gaa gaa ggc att cct gca gtc cgc atg ttc ggc atg att gct cac			691
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His			
185	190	195	
gaa gaa gtt ttc ttc ggc att cag ggt cag att ttc acc ttc cag ctg			749
His Gln Val Ile Ile Gly Thr Gln Gly Gln Thr Thr Thr Ile Lys Gln			
200	205	210	
gaa tcc tat gat cgc aac tca tct gca cca ggc gtc ttg gtc ggt gtc			797
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val			
215	220	225	
gga aac att gca cag cac cca ggc tta gtc gta gga ctt gag cat tcc			835
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr			
230	235	240	245
cta ggc ctg taaaggctca ttccagcaga ggc			867
Leu Gly Leu			

(210) 34
 (211) 248
 (212) PRT
 (213) Corynebacterium glutamicum

(400) 34
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 20 25 30
 Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
 35 40 45
 Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
 50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
 65 70 75 80
 Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
 85 90 95
 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
 100 105 110
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
 115 120 125
 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
 130 135 140
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
 145 150 155 160
 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
 165 170 175
 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
 180 185 190
 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
 195 200 205
 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
 210 215 220
 Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
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 Gly Leu Glu His Tyr Leu Gly Leu
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 <223> EXA00864

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 Val Ala Glu Gln Val
 1 5
 aaa ttg agc gtg gag ttg ata ggc tgc agt tct ttt act cca ccc gct 163
 Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
 10 15 20
 gat gtt gag tgg tca act gat gtt gag ggc ggc gaa gca ctc gtc gag 211
 Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
 25 30 35

ttt ggg ggt cgt gcc tgc tac gaa act ttt gat aag cgg aac cct cga 259
 Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
 40 45 50

act gct tcc aat gct ggg tat ctg cgc cac atc atg gaa gtg ggg cac 307
 Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
 55 60 65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att 355
 Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
 70 75 80 85

tat cgg tcc ggg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc 403
 Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
 90 95 100

tat caa ctg tct cag cgt ttc gtg cac agc gga gaa tgg gaa gta gtg 451
 Ser Gln Ser Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
 105 110 115

gtg ccc att ctg atc gat gaa gat cag cag ttg cgt gaa ctt ttc atg 499
 Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met
 120 125 130

cac gcc tta gat gat tct cgg ttc act ttc aat cac ctg ctt aat gag 547
 His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
 135 140 145

ctg gaa gaa aaa ctt ggt gat gaa cgg aat gca ctt tta agg aaa aag 595
 Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
 150 155 160 165

cag gct cgt caa gca gct cgt gct gtg ctg ccc aac gct aca gag tcc 643
 Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
 170 175 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc 691
 Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
 185 190 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta ggg gta 739
 Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
 200 205 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat 787
 Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
 215 220 225

ttt gag att gaa act ttg gca gac gga tgg caa atg gca aca agc cgg 835
 Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
 230 235 240 245

tat gtc atg gac ttt taacgcaaaag ctcacaccca cga 873
 Tyr Val Met Asp Phe
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<210> 36
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<213> Corynebacterium glutamicum

<400> 36

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Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
  35           40           45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
  50           55           60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
  65           70           75           80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
  85           90           95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
 100           105           110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
 115           120           125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
 130           135           140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
 145           150           155           160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
 165           170           175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
 180           185           190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
 195           200           205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
 210           215           220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
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Met Ala Thr Ser Pro Tyr Val Met Asp Phe
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<211> 608

<212> DNA

<213> Corynebacterium glutamicum

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<222> (69)..(608)

<223> RXA02843

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tggacgtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc 110

Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser

1

5

10

acc ggc gar ttc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158

Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp

15

20

25

30

cag tcc ggc ctg aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206

Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val

35

40

45

acc cgc aca att gtg acc aca act atc gac acc gac gca ggc ccc acc 254

Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr

50

55

60

gac acc tac gat gca tgg ctg cgc ctt cac ctg ctg tcc cag cgc gtt 302

Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val

65

70

75

tcc cgc ctt cag acc atc aac cta gaa ggc att tcc ggc ctg ctg aac 350

Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn

80

85

90

aat ttc gtc ttt acc aac ttc gga ctt tgc gaa att gar agt ttc gaa 398

Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala

95

100

105

110

ctc acc cgc ggc cgc ctg tca cgc cga ggc caa gtt acc gtt tat agc 446

Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser

115

120

125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcc ggc gtg 494

Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val

130

135

140

cgg atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac cag gca gar 542

Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp

145

150

155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acc 590

Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr

160

165

170

ctc ggc gct tcc atg gtt 608

Leu Gly Ala Ser Met Val

175

180

<210> 38

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<213> *Corynebacterium glutamicum*

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Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly

1

5

10

15

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gctccgcatg aaagagatgt cccggaatca tcattctaagt atg cat ctc ggt aag 115
Met His Leu Gly Lys
1 5
ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
10 15 20
acc aac atc cgc gta gct atc gtg gcc tac gga aac ctg gga cgc agc 211
Thr Asn Ile Arg Val Ala ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
25 30 35
gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259

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Val	Glu	Lys	Leu	Ile	Ala	Lys	Gln	Pro	Asp	Met	Asp	Leu	Val	Gly	Ile		
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ttc	tcc	ccc	ggg	gac	acc	ctc	gac	aca	aag	acg	cca	gtc	ttt	gat	gtc	307	
Phe	Ser	Arg	Arg	Ala	Thr	Leu	Asp	Thr	Lys	Thr	Pro	Val	Phe	Asp	Val		
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gcc	gac	gtg	gac	aag	cac	gcc	gac	gac	gtg	gac	gtg	ctg	ttc	ctg	tgc	355	
Ala	Asp	Val	Asp	Lys	His	Ala	Asp	Asp	Val	Asp	Val	Leu	Phe	Leu	Cys		
	70				75					80					85		
atg	ggc	tcc	gac	acc	gac	atc	cct	gag	cac	gca	cca	aag	ttc	gag	cac	403	
Met	Gly	Ser	Ala	Thr	Asp	Ile	Pro	Glu	Gln	Ala	Pro	Lys	Phe	Ala	Gln		
				90				95						100			
ttc	ggc	tga	acc	gta	gac	acc	tac	gac	aac	cac	cgc	gac	atc	cca	ggc	451	
Phe	Ala	Cys	Thr	Val	Asp	Thr	Tyr	Asp	Asn	His	Arg	Asp	Ile	Pro	Arg		
			105					110					115				
cac	cgc	cag	gtc	atg	aac	gaa	gcc	gcc	acc	gca	gcc	ggc	aac	gtt	gca	499	
His	Arg	Gln	Val	Met	Asn	Glu	Ala	Ala	Thr	Ala	Ala	Gly	Asn	Val	Ala		
			120				125					130					
ctg	gac	tct	acc	ggc	tgg	gat	cca	gga	atg	ttc	tcc	atc	aat	agg	gtc	547	
Leu	Val	Ser	Thr	Gly	Trp	Asp	Pro	Gly	Met	Phe	Ser	Ile	Asn	Arg	Val		
	135					140						145					
tac	tca	gtt	tta	gtc	tta	gtt	gat	gat	cgt	cag	cac	aat	ttc	tgt	gtt	595	
Tyr	Ala	Ala	Ala	Val	Leu	Ala	Glu	His	Gln	Gln	His	Thr	Phe	Trp	Gly		
	150				155					160				165			
cca	ggt	ttg	tca	cag	ggc	cac	tcc	gat	gct	ttg	cga	cgc	atc	cct	ggc	643	
Pro	Gly	Leu	Ser	Gln	Gly	His	Ser	Asp	Ala	Leu	Arg	Arg	Ile	Pro	Gly		
			170						175					180			
gtt	caa	aaa	cca	gtc	cac	tac	acc	ctc	cca	tcc	caa	cac	acc	ctg	caa	691	
Val	Gln	Lys	Ala	Val	Gln	Tyr	Thr	Leu	Pro	Ser	Glu	Asp	Ala	Leu	Glu		
			185					190					195				
aag	ggc	cgc	cgc	ggc	gaa	gcc	ggc	gac	ctt	acc	gga	aag	caa	acc	cac	739	
Lys	Ala	Arg	Arg	Gly	Glu	Ala	Gly	Asp	Leu	Thr	Gly	Lys	Gln	Thr	His		
		200					205					210					
aag	cgc	caa	tgc	ttc	gtg	gtt	gcc	gac	ggg	gcc	gat	cac	gag	cgc	atc	787	
Lys	Arg	Gln	Cys	Phe	Val	Val	Ala	Asp	Ala	Ala	Asp	His	Glu	Arg	Ile		
	215					220					225						
gaa	aac	gac	atc	cgc	acc	atg	cct	gat	tac	ttc	gtt	ggc	tac	gaa	gtc	835	
Glu	Asn	Asp	Ile	Arg	Thr	Met	Pro	Asp	Tyr	Phe	Val	Gly	Tyr	Glu	Val		
	230					235					240				245		
gaa	gtc	aac	ttc	atc	gac	gaa	gca	acc	ttc	gac	tcc	gag	cac	acc	ggc	883	
Glu	Val	Asn	Phe	Ile	Asp	Glu	Ala	Thr	Phe	Asp	Ser	Glu	His	Thr	Gly		
			250						255					260			
atg	cca	cac	ggt	ggc	cac	gtg	att	acc	acc	ggc	gac	acc	ggt	ggc	ttc	931	
Met	Pro	His	Gly	Gly	His	Val	Ile	Thr	Thr	Gly	Asp	Thr	Gly	Gly	Phe		
			265					270					275				
aac	cac	acc	gtg	gaa	tac	atc	ctc	aag	ctg	gac	cga	aac	cca	gat	ttc	979	
Asn	His	Thr	Val	Glu	Tyr	Ile	Leu	Lys	Leu	Asp	Arg	Asn	Pro	Asp	Phe		

280 285 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag 1027
 Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys
 295 300 305

cag cag ggc caa agc gga gct ttc acc ttc ctc gaa gtt gct cca tac 1075
 Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr
 310 315 320 325

ctg ctc tcc cca gag aac ttg gac cat ttc atc gaa cgc gac gtc 1120
 Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
 330 335 340

taatttagct cagggggcaa gga 1143

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 <213> Corynebacterium glutamicum

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 21 25 30

Asn Leu Gly Arg Ser Val Gln Lys Leu Ile Ala Lys Gln Pro Asp Met
 35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
 50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65 70 75 80

Val Leu Phe Ile Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
 85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
 100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
 115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
 130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
 145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
 165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
 180 185 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
 195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
245 250 255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
275 280 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
290 295 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
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Ala Arg Asp Val
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<223> FRXA00352

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Met His Leu Gly Lys
1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
40 45 50

ttc tgg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
55 60 65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg atg ttc atg tgc 355
 Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
 70 75 80 85
 atg gcc tcc gcc acc gac atc cct gag cag gca cca aag ttc gag cag 403
 Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
 90 95 100
 ttc gcc tgg acc gta gac acc tac gac aac caa cgc gac atc cca cgc 451
 Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
 105 110 115
 caa cgc cag atc atg aac gaa gac gcc acc gca acc gac aac gtt gca 499
 His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
 120 125 130
 ctg gcc ttc acc gtt tgg gtt cca gga atg ttc tcc atc aac gtt gtc 547
 Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
 135 140 145
 tac gaa gtt gca gta tta ttc gag cag cag cag cag aac ttc ttt gga 595
 Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
 150 155 160 165
 cca ggt ttc tca cag ggt cag ttc gag ttt ttg gaa cgt atc ctt ggt 643
 Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
 170 175 180
 gtt caa aag gca gtc cag tac acc ttc cca tcc gaa gac gcc atg gaa 691
 Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
 185 190 195
 aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac 739
 Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
 200 205 210
 aag cgc caa tgc ttc gtg gtt gcc gac ggc gcc gat caa gag cgc atc 787
 Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
 215 220 225
 gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc 835
 Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
 230 235 240 245
 gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag caa acc ggc 883
 Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
 250 255 260
 atg caa caa ggt ggc caa gtg att acc acc ggc gac acc ggt ggc ttc 931
 Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
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 aac caa acc gtg gaa tac atc ttc aag 958
 Asn His Thr Val Glu Tyr Ile Leu Lys
 280 285

<210> 42
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<213> Corynebacterium glutamicum

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35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
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Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
100 105 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
180 185 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
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Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
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Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys
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<223> RNA006972

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Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
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acc gtg cgc caa gaa gac ggc ggt ggc acc atc gct ggt gtg act ctg 144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
35 40 45

act gac ctc gct gaa gaa tac gta acc cca cta ttc gta gac gag 192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
50 55 60

gac gat ttc act tcc cgc tgt cgt gac atg gct acc gaa ttc ggt gaa 240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
65 70 75 80

caa ggc aat gtg ctc tac gta tct aac ggt ttc ctg acc atg atc att 288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
85 90 95

gaa ctt tgg gtc gat gaa gaa ggt cta gaa ctg gac att gaa tcc atc 336
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
100 105 110

aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc 384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
115 120 125

acc gag cac ggc aac aac aaa ggc gta gag ttc ctg cgc gag ttg gtt 432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
130 135 140

caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa 480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
145 150 155 160

ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg 528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
165 170 175

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc 576
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
180 185 190

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Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
195 200 205

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ttc aag ctg gaa gaa gaa cgc gta ttg ggc ctg tac tca cag atc cac Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His 245 250 255	768
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ggc att gcc tat acc gaa gct gaa gaa cca ctc aac gtc gaa gaa gtt Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val 275 280 285	864
gct tcc gac ttc ttc ttc acc gaa gtc gaa aaa atg gaa gta gaa cta gcc Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly 290 295 300	912
atc gac gaa cca acc gta ctt gta gag ccc ggc ggc ggt atc gaa ggc Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly 305 310 315 320	960
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gta gta tcc gcc ttc gcc gaa gga gac cca gta agc acc gcc atc gta Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val 370 375 380	1152
ggc tcc cac tgc gaa tcc gcc gat atc ctg atc aac gat gaa atc tac Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr 385 390 395 400	1200
cca tct gac atc acc agc gcc gac ttc ctt gca ctc gca gcc acc gcc Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly 405 410 415	1248
gca tac tgc tac gcc atg agc tcc gcc tac aac gcc ttc aca cgg ccc Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro 420 425 430	1296
gcc gtc gta tcc gta gcc gct gcc agc tcc gcc ctc atg ctg cgc cgc Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg 435 440 445	1344
gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgaacgctga Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala	1392

450

455

ccc

1400

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 Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
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 Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
 65 70 75 80
 Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
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 Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
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 Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
 115 120 125
 Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
 130 135 140
 Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
 145 150 155 160
 Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
 165 170 175
 Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
 180 185 190
 Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
 195 200 205
 Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
 210 215 220
 Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
 225 230 235 240
 Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
 245 250 255
 Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
 260 265 270

Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
 275 280 285

Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
 290 295 300

Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
 305 310 315 320

Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
 325 330 335

Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
 340 345 350

Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
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Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
 370 375 380

Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
 385 390 395 400

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
 405 410 415

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
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Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
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 Met ile Pro Lys Pro
 1 5

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 Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
 10 15 20

aag att cgg tcc gac aag gat ctt tcc gaa ctt agg aca gtt cta aaa 211
 Lys ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys

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Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu			
40	45	50	
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Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu			
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cac gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat ccc tta			355
Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu			
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ggt cgg gaa atg gaa aga tta ggt ttc cgc cca cca tcc gaa agt ttt			403
Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe			
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gaa tac ctg cca gaa ctg cta gaa tct cga ctg gta gac atc aat ccc			451
Gln Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His			
105	110	115	
atg aat ggt ggt cgg gaa tta ctg atc gat tta gtt cgt gaa att gaa			499
Leu His Arg Gly Arg Glu Arg Leu Thr Asp Leu Val Arg Glu Leu Glu			
120	125	130	
ata aat tta ctg ata cca gct att att ctt cgt cgc cca gta gta gta cca			547
Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro			
135	140	145	
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cct cgg aat cgg cgg tta gat gta gag gct gac ggc acc gtt cca ggg			643
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly			
170	175	180	
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Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu			
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200	205	210	
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Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu			
230	235	240	245
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Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser			
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cct gtg aat gta ctg cat tca ggt tct atg cct cgt aat ata aat gag			931
Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu			
265	270	275	

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Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp	
295 300 305	
acc agt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg	1075
Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val	
310 315 320 325	
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330 335 340	
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Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile	
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Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val	
375 380 385	
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Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe	
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Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly
      35             40             45
Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
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Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
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Val	Arg	Glu	Leu	Glu	Ile	Thr	Val	Val	Ile	Asp	Ala	Val	Leu	Pro	Pro	
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Arg	Asn	Ile	Asn	Glu	Leu	Val	Asp	Ala	Gly	Ile	Gln	Met	Gly	Val	Asp	
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Leu	Ser	Ala	Ala	Ile	Lys	Pro	Asp	Arg	Leu	Leu	Ala	Leu	Ala	Ile	Glu	
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	370					375					380					
Pro	Asp	Pro	Ala	Val	Leu	Pro	Pro	Thr	Arg	Phe	Gly	Glu	Arg	Ala	Ala	
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Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
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 His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr
 450 455 460
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 465 470 475 480
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 515 520 525
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 Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu
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 Met Asn Pro Ile Gln
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 Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro
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 gag aac gca aac gaa ggc ggt gaa gta ttc gtg aac aca ggc tgg caa 307
 Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys
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 Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala
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 Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp
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 Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val
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Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly
 215 220 225

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 230 235 240 245

gga gga gaa atg atc ctc ctc gat gag ata ccc att gag aca cgg atg 885
 Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met
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 265 270 275

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 <212> PRT
 <213> Corynebacterium glutamicum

<214> 48
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Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
 180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
 195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
 210 215 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
 225 230 235 240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
 245 250 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
 260 265 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
 275 280 285

Arg Pro
 290

210 49
 211 1626
 212 DNA
 213 Corynebacterium glutamicum

220
 221 CDS
 222 (101)..(1603)
 223 RNA30241

400 49
 ggtcttcagc atttctaaa aattcattcgt cacttgattt attggcccca agatttagcg 60

aagtttagcg aatttcgcgt acgtcaacta cgttaaattga gtg aat act caa tca 115
 Val Asn Thr Gln Ser
 1 5

gat tct gag ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct 163
 Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser
 10 15 20

att aga acc ctg atc gcg ctg atc atc gga tgg acc gtc ggc gcg gga 211
 Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
 25 30 35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg 259
 Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
 40 45 50

atg ctg atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg 307
 Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
 55 60 65

ttc gag ttc cat gtt att gac cgc cgt aaa cct ctc ctg gat tct ggc 355
 Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
 70 75 80 85

gtc tac gca tat ggc cgt gtt gga tgg ggc gat tat gta ggt ttc tcc	403
Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser	
90 95 100	
cac gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac	451
Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr	
105 110 115	
gca acg tta ttt ttc tcc acg ttg ggc cac tac gta cgg ctg ttt tcc	499
Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser	
120 125 130	
caa gat cat caa ttt gty tca ggc ttg gca gtt agc gat ttg acc tgg	547
Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp	
135 140 145	
ctg gta ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg	595
Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu	
150 155 160 165	
ala acg gta acc caa gty ggc aaa att ctg cat ctg ttg tgc ttc att	643
Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile	
170 175 180	
atc att gtt gca ttc ttc ggc ttt agt tgg gag aag ttc act gtt gat	691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp	
185 190 195	
tta tgg ggc cgt gat ggt ggc gty ggc agt att ttt gat cac gta ggc	739
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg	
200 205 210	
ggc atc atg gta tac acc gty tgg gta ttc atc ggt atc gaa gtt gca	787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala	
215 220 225	
tgg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct	835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala	
230 235 240 245	
acc gta att ggt ttt gty gct gtt ctc ctt ttg ctg gta tgg att tat	883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Val Ser Ile Ser	
250 255 260	
tgg ctg agc ttc ggt gta ctg acc caa caa gag ctg gct gcc tta caa	931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro	
265 270 275	
gat aat tcc atg ggc tgg gta ctc gaa gct gtt gtt ggt caa tgg ggt	979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly	
280 285 290	
gcc gaa ttg att tgg ttg ggt ctg tgt ctt tgg gtt ctt ggc gcc tat	1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr	
295 300 305	
gtg tcc tgg cag atg ctc tgc gca gaa caa ctg ggc ttg atg gca atg	1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met	
310 315 320 325	

gat ggc ctc att cca agc aaa atc ggg ggc atc aac agc cgc ggt gct 1123
 Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala
 330 335 340

goc tgg atg gct cag ctg atc toc aac atc gtg att cag att ttc arc 1171
 Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
 345 350 355

atc att ttc ttc ctc aac gag aac aac tac gtc toc atg gtg cca ttg 1219
 Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu
 360 365 370

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg 1267
 Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
 375 380 385

gtc atc ctg gga acg cgt gga aaa gga atc aac cgc cca cat gtc gac 1315
 Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
 390 395 400 405

aca cgt ttc gat gat toc ggt cca gag atc ttc cgc gga gaa gac cgc 1365
 Thr Arg Phe Asp Asp Ser Gly Pro Gln Ile Ser Arg Arg Gln Asn Arg
 410 415 420

caa cgc ctc atc gtc ggt tta gta gca acg gtc tat tca gtc tgg ctg 1411
 Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
 425 430 435

tat caa gct gga gaa cag cag ttt gtc atc ttc gaa gac att cag atg 1459
 Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
 440 445 450

ctc ccc ggc tta atc ccc tat gtc tgg tca agg att tat gtc ggc gaa 1507
 Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
 455 460 465

cag gtg ttt aac cgc ttt gaa atc ggc gtc gtt gtt gtc ctg gtc gct 1555
 Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
 470 475 480 485

gct gcc agc ggc ggc gtt att ggt ttg gtc aac gga tca cta tgg ctt 1603
 Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
 490 495 500

taaacaccca aaccttcctg cta 1626

<210> 50
 <211> 501
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 50
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 Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
 20 25 30
 Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
 35 40 45

Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
 50 55 60
 Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
 65 70 75 80
 His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
 85 90 95
 Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
 100 105 110
 Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
 115 120 125
 Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
 130 135 140
 Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
 145 150 155 160
 Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
 165 170 175
 Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Ile Ser Trp Gln
 180 185 190
 Lys Ile Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
 195 200 205
 Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
 210 215 220
 Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
 225 230 235 240
 Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
 245 250 255
 Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
 260 265 270
 Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
 275 280 285
 Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
 290 295 300
 Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
 305 310 315 320
 Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
 325 330 335
 Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
 340 345 350
 Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
 355 360 365

Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
 370 375 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr
 385 390 395 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Gln Ile Ser
 405 410 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val
 420 425 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe
 435 440 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Tyr Thr Arg
 450 455 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val
 465 470 475 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
 485 490 495

Gly Ser Leu Ser Leu
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<212> 51
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)...(799)
 <223> RXA(1394

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ccattttact taagtacttc cataggtcac gatgggtgac atg gaa atc ttc att 115
 Met Glu Ile Phe Ile
 1 5

aca ggt ctg att ttg ggg gcc agt ctt tta ctg tcc atc gga ccg baq 163
 Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
 10 15 20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg 211
 Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
 25 30 35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc gcc 259
 Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
 40 45 50

acc ttg gcc gtt gat att ttg tcc aat gcc gcc ccg atc gtg ctc gat 307
 Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
 55 60 65

att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg 355
 Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
 70 75 80 85

 gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att 403
 Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
 90 95 100

 gaa gaa aca gaa cca acc ggg ccc gat gac acg cct ttg ggc ggt tgg 451
 Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser
 105 110 115

 tgg gtg acc acg gac acg cgc aac cgg gtg cgg gta gag gta agc gtc 499
 Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
 120 125 130

 gat aag aag cgg gtt tgg gta aag cca atg ttg atg gca atc atg atg 547
 Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
 135 140 145

 acc tgg ttg aac cgg aat ggt tac tta gac gcg ttt gtg tta atc gcc 595
 Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
 150 155 160 165

 ggc gtc ggc gcg caa tac gcc gac aac gga cgg tgg att ttc gtc gct 643
 Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
 170 175 180

 ggc gcg tta ggc gta agc atg atc tgg tta cgg atg gta gta tta gcc 691
 Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
 185 190 195

 aca gca caa tgg tta gcc cgg atg tta ggc cca aac gta tta gca tgg 739
 Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
 200 205 210

 atc aac gtc gtc gta gca gtt gta atg acc gca ttg gcc atc aac atg 787
 Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu
 215 220 225

 atg ttg atg ggt tagttttcgc gggtttttggga atc 822
 Met Leu Met Gly
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<210> 52

<211> 233

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 52

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 Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
 35 40 45

 Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala

50

55

60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu
65 70 75 80

Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu
85 90 95

Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr
100 105 110

Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg
115 120 125

Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu
130 135 140

Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala
145 150 155 160

Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg
165 170 175

Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro
180 185 190

Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro
195 200 205

Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala
210 215 220

Leu Ala Ile Lys Leu Met Leu Met Gly
225 230

<210> 53

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA00865

<400> 53

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tttaaccccc aaatgagggga agaaggtaac ctggaactct atg agc aca ggt tta 115
Met Ser Thr Gly Leu
1 5

aca gct aag acc gga gta gag caa ttc ggc acc gtt gga gta gca atg 163
Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met
10 15 20

gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211
Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg
25 30 35

gaa gtc geg get tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc	259
Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu	
40 45 50	
gag ggc acc act ggt gaa tcc cca aag ada aca gac get gaa aia cta	307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu	
55 60 65	
gaa ctg ctg aag gac gtt cgt gag gaa gtt ggg gal cgg ggg aag ctg	355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu	
70 75 80 85	
atc gac gtt gtc gga acc aac aac aag agg aca tct gtc gaa ctt ggg	403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala	
90 95 100	
gaa gct gtt gtt tat gct ggt gaa gac ggt ctt tta ctt gta act gct	451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro	
105 110 115	
tat tat tcc aag cgg acc caa gac gga tta ctg gaa cac tta gtt gaa	499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His His Gly Ala	
120 125 130	
att gct gaa gaa aca gag gtt cca att tgg cta tat gac att act ggt	547
Ile Ala Ala Ala Thr Glu Val Pro Ile Tyr Leu Tyr Asp Ile Pro Gly	
135 140 145	
agg tca gtt att gaa att gag tct gat att atg gaa cgg ctg att gaa	595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu	
150 155 160	
tta ctt acc att ttg ggt gtc aag gac gaa aag gtt gac ctg gtt gaa	643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala	
165 170 175	
gac aag tca ttg atc aaa gaa aag gaa ctt gac tgg tat tca ggc gat	691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp	
180 185 190 195	
gac cca cta aac ctt gtt ttg ctt gat ttg ggc gga tca ggt ttc att	739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile	
200 205 210	
tcc gta att gga cat gaa gcc ccc aca gaa tta cgt gag ttg tac aca	787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr	
215 220 225	
agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa	835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys	
230 235 240 245	
cta tca cgg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg	883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu	
250 255 260	
gaa aac gtt gtt ctg cgt ctg cag ggc atc aac gta gga gat ctt cga	931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg	
265 270 275	
att aca att att gtt cca att gag cag gaa att gag gat ctc cga gaa	979

Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu
 280 285 290

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattccaga aat 1026
 Asp Met Lys Lys Ala Gly Val Leu
 295 300

<210> 54
 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 54
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 20 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
 35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
 50 55 60

Ala Ala Glu Lys Leu Gln Leu Leu Lys Ala Val Arg Glu His Val Gly
 65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
 85 90 95

Ser Val Thr Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Arg Gly Leu
 100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
 115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
 130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
 145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
 165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
 180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
 195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
 210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
 225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
 245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
275 280 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
290 295 300

<210> 55

<211> 1671

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (131)...(164-)

<223> RXSF2031

<400> 55

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Met Ser Glu Asn Ile
1 5

atg gga gtt caa gta att ggt atc gaa gat at' gtc atg gac tgg aac 163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
10 15 20

atc ctg gac aag tat tac caa gaa caa caa att ttc aac ctg gat cag 211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
25 30 35

tgg gct gaa cgc tac caa ttg gaa gtg ggc acc aca cgc ctg gga gaa 259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
40 45 50

aac gaa ctg acc caa ggg atg ctg cag ttg gta aaa ctg gac caa gat 307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
55 60 65

cgc ctg gtc gaa cag gta gaa gtc cgc acc gtt atc ccc gat ctg tet 355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
70 75 80 85

caa cct caa gta gac gcg cac gat gtt tac ctg cgc ctg cac ctg ctt 403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
90 95 100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
105 110 115

gag ctg ctg tcc gac ttg gtt tgg aca aac aac ggc cct tgg ctt cct 499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
120 125 130

gaa aac ttt gag ttg gtt ggt gct ctg cgg tcc cgc gga ctg atc 547

Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
 135 140 145

cac gtc tac tgt gtg gac cgt att ccc cgc atg gtc gac tat gtg gtt 595
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
 150 155 160 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
 170 175 180

tac att gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
 185 190 195

aac tcc ggc acc tgg ggt gac gca aag gtg gaa ggc cgc ctg agt tcc 739
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
 200 205 210

ggt atg atc atc ggt gaa ggt tcc aac att gga ctg tct tct act att 787
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
 215 220 225

cag tcc ccg aga gat gaa cag cgc cgt cgt ttc ccg tcc agg atc gac 835
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245

aac aac tgc aac ttt ggt gtc agt tcc gga atc tcc gga ttc att ttc 887
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260

gaa aac aat tgc gac atc gaa aat aac att gtc ttc gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305

cca att gcc cgc ctc aaa gct tgaccattt tcataaccag tgc 1071
 Pro Val Ala Arg Leu Lys Ala
 310 315

<210> 56

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
 1 5 10 15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
 20 25 30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

35	40	45
Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val 50 55 60		
Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val 65 70 75 80		
Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu 85 90 95		
Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His 100 105 110		
Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys 115 120 125		
Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg 130 135 140		
Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met 145 150 155 160		
Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg 165 170 175		
Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu 180 185 190		
Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu 195 200 205		
Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly 210 215 220		
Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu 225 230 235 240		
Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile 245 250 255		
Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val 260 265 270		
Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg 275 280 285		
Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu 290 295 300		
Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala 305 310 315		

<210> 57

<211> 1296

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1273)

<223> RNS02157

<400> 57

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caacgttttt agaaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
Met Ser Thr Leu Glu
1 5

aat tgg cca cag gtc att att aat acg tac agc aac cca gtc gag 163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc aat aat gac cag ggc aat ttc 211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
25 30 35

tac atc gac tta ctc ggc ggc atg gca gtc aat gtc tta tta aat ggc 259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
40 45 50

aa tgg gta atc atc aag ggc gtc aat aat aat atc ggc aac att aat 307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
55 60 65

aat gtc tac aat tta tta gca tta agc aat gta gtc aat tta gta aat 355
His Val Ser Asn Leu Ile Ala Ser Arg Pro Val Val Glu Val Ala Glu
70 75 80 85

gac ttc atc aag ggt tta tta gtc gtc gac gac aat aat ttc ggc ggc aac 403
Gln Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
90 95 100

acc cgg gtt ttc ttc tgc aac tgc ggc gca gaa gca aac gag ggt ggt 451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
105 110 115

ttc aag att gca cgc ttg aat ggt cgt tcc cgg att ctg ggt gca gtt 499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
120 125 130

aat ggt ttc cac ggc cgc acc atg ggt tcc atc gag ctg aat ggc cag 547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
135 140 145

cca gac aag cgt gaa ggc ttc ctg cca atg cca agc ggt gtg gag ttc 595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn
170 175 180

cca aag gac gtg ggt ggt atc ttc ctc gag cca atc cag ggt gaa acg 691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr
185 190 195

ggc gtt gtt cca gca acc gaa gga ttc ctc aag gca gtg cgc gag ctg 739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu
200 205 210

tgc gat gag tac gcc atc ttg atg atc acc gat gaa atc cag act gcc 787
 Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly
 215 220 225
 ggt gcc cgt acc gcc gat ttc ttt gca cat cag cac gat gcc gtt gtt 835
 Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
 230 235 240 245
 acc gat atg gag acc atg gcc aag gga ctt gcc gcc ggt ctt acc atc 843
 Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
 250 255 260
 ggt gat tgt tgg gcc act gcc cgt gca gct gaa ctg atg acc gca gcc 931
 Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
 265 270 275
 aag cac ggt acc act ttc ggt ggt aac cca gtt ggt tgt gca act gcc 979
 Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
 280 285 290
 aag gca atg ctg tct gtt atc gat gac gct ttc tgc gca gaa gtt gct 1027
 Cys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
 295 300 305
 ggt aag ggt gag ctg ttc aag gaa cca ctt gcc aag gtt gat gcc gtt 1103
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325
 gcc gat gtt gtt ggt aag gcc ttg atg ttg gcc gtt ttt gtt gcc gtt 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340
 aag gtc gca aag gaa gct ctt ctt gat ggt ttt aag cac gcc att att 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355
 tgg aat gca cag gag gac aac att atc cgt ttg acc ccg ccg ctg gtc 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385
 atc gca taaaggactc aaacttatga ctt 1296
 Ile Ala
 390

<110> 58

<111> 391

<112> PRT

<113> Corynebacterium glutamicum

<400> 58

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
 1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
 115 120 125
 Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Thr Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Thr Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350

Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
355 360 365

Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
370 375 380

Ala Ile Ala Glu Thr Ile Ala
385 390

<210> 59

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> K001473

<400> 5'

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ggaaatagt tgaatccaa agactcaga aagcgaatc atg agt aat gtt gga 115
Met Ser Asn Thr Ala
1 5

ggc ccc ggc ggg agt tcc cat cag gca gat gtt tgg tct aat cca aag 165
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys
10 15 20

gca cag aat ttc gga cca tct gcc aac agg ctt ttc gga aat cta ggc 211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Ile Gly Ile Leu Gly
25 30 35

gat gag agt aac acc tta att ttc gtt atc ttc cta gcc gtc ctg agc 259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser
40 45 50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac 307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn
55 60 65

gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt ggc tca 355
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser
70 75 80 85

aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag 403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln
90 95 100

gct tcc atg atg gaa gac atg aac ctt gtt cca gcc tca gcc att gat 451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp
105 110 115

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc 499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu
120 125 130

atc ggt agc ctg ttg tgg ttg ttc cag gcg cgg atg ctc aac cgc atc 547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile

135	140	145	
gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc			595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile			
150	155	160	165
cac cgg cta cgg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg			643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu			
	170	175	180
ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa			691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln			
	185	190	195
caa acc ctg tca gag gag atc aat tcc cta ctg acc gta atc ggt gtg			739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val			
	200	205	210
tgg gta atg atg ctt atc atc tcc cca cgg ctc gca ctt ggt gag ctg			787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu			
	215	220	225
gta tcc att cgg gtc acc atc gtg gtc aat gtg gtg gtt gag agc cgt			835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg			
	230	235	240
tcc cag aaa atc ttt cgg gaa gag tgg aag ttt acc ttt att ctg aat			883
Ser Gln Lys Leu Phe Ala Gln Gln Trp Lys Gln Thr Gly Ile Leu Asn			
	250	255	260
gag cgg ctg gag gaa acc tac tct ggc cag tcc gtg gtt aag gtt ttc			931
Ala Arg Leu Glu Gln Thr Tyr Ser Gly His Ala Val Val Lys Val Phe			
	265	270	275
gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa got			979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala			
	280	285	290
tgt gta caaggcagc ttgggtgcgc agt			1008
Cys Val			
	295		

<210> 60

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met	Ser	Asn	Thr	Ala	Gly	Pro	Arg	Gly	Arg	Ser	His	Gln	Ala	Asp	Ala
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Ala	Pro	Asn	Gln	Lys	Ala	Gln	Asn	Phe	Gly	Pro	Ser	Ala	Lys	Arg	Leu
		20					25					30			

Phe	Gly	Ile	Leu	Gly	His	Asp	Arg	Asn	Thr	Leu	Ile	Phe	Val	Ile	Phe
	35				40						45				

Leu	Ala	Val	Leu	Ser	Val	Gly	Leu	Thr	Val	Leu	Gly	Pro	Trp	Leu	Leu
	50				55						60				

Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
65 70 75 80

Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala
85 90 95

Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro
100 105 110

Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val
115 120 125

Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg
130 135 140

Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu
145 150 155 160

Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile
165 170 175

Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile
180 185 190

Gly Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu
195 200 205

Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu
210 215 220

Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val
225 230 235 240

Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln
245 250 255

Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala
260 265 270

Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu
275 280 285

Glu Gln Asn Gln Ala Cys Val
290 295

<210> 61

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(426)

<223> RXC00861

<400> 61

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Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
1 5 10 15

cat atg gct gag ctg tct cga atg gag cgt cgt gag cac cga cag atc 95
 Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca 144
 Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc 192
 Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

ggt aca act gtt gtt acc ggt cgc gac ggc aag gag cac aac tgg ggc 240
 Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

cat cgt tct tct gaa gag ctg ttg ttt ttg ttt aac gct gtt cgt cgt 288
 His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

aac aac gtt atc cgt ggc cac ggc gaa tgg cgc cac ctg cac acc aac 336
 Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

aac aac ctg act atc tcc act ggt gtt aac cgc gac aac gtt ttg ctt 384
 Lys Glu Leu Ala Thr Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
 115 120 125

gaa aac aac ggt gtt gtt gtt att atg gtc aac gtt tgg gta 432
 Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 62

<211> 142

<212> FRT

<213> Corynebacterium glutamicum

<400> 62

Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
 1 5 10 15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
 20 25 30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
 35 40 45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
 50 55 60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
 65 70 75 80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
 85 90 95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
 100 105 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu

115

120

125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
 130 135 140

<210> 63
 <211> 1066
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1066)
 <223> R0000866

<400> 63
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ctctcgaac aacatgaaa aaagctggag tctctaacat atg aat gat tcc cga 115
 Met Asn Asp Ser Arg
 1 5

aat cga ggc agc aag gtt acc cgt aag ggc cgc acc cga ggt ggt 163
 Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Gln Ala Gly
 10 15 20

cag gaa aac cat atg gat acc cgt ggc ttc aag gaa cca gat ggt ttc 211
 Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser
 25 30 35

tct aac cag acc ggt gta aaa ggt gag acc ggc gga aac gac aat cgg 269
 Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg
 40 45 50

gat ggt ggc caa ggt ggt caa gga tcc caa gat tct cag ggt tcc cag 307
 Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln
 55 60 65

aac ggt caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355
 Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn
 70 75 80 85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403
 Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly
 90 95 100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451
 Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln
 105 110 115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499
 Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys
 120 125 130

tcc atg cag ggt ggc gat ctg acc cag cgt ctg cca gag cca cca aag 547
 Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys
 135 140 145

gca cgc cca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa 595
 Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu

150	155	160	165	
atc ggt cgc aag atg acc gtg ttt gag tac aac aac cgt ctg etc atc				643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile	170	175	180	
gtg gac tgt ggt gtg etc ttc cca tct tca ggt gag cca ggc gtt gac				691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp	185	190	195	
ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc				739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val	200	205	210	
gat gca ttt gtg gtt act cac gga cac gaa gac cac att ggt gat att				787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile	215	220	225	
cca tga tta cta aac ctg cgc aac gat atc cca att tta gca tta cgt				835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg	230	235	240	
tta cca tta gct ctg att gga gct aag tgt aag gaa cac cgt cag att				883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg	245	250	255	
cag cag tta atg gag gtt ctc cag cag tta gat gac gat cgt gga cag				931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro	260	265	270	
tta cac att cgt ttc ttt ggt gtt aac cac tta atg cca gat tta ctt				979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu	275	280	285	
ggt ttt ggt atc aag act cct ggt ggt ttg gtc atc cac acc ggt gac				1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp	295	300	305	
atc cag ctg gat cag act cct cct gat gga cgc cca act				1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr	310	315	320	

<210> 64

<211> 622

<212> PRT

<213> Corynebacterium glutamicum

<400> 64

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Pro	Pro	Glu	Ala	Gly	Gln	Glu	Asn	His	Leu	Asp	Thr	Pro	Val	Phe	Gln
		20						25					30		

Ala	Pro	Asp	Ala	Ser	Ser	Asn	Gln	Ser	Ala	Val	Lys	Ala	Glu	Thr	Ala
		35					40					45			

Gly	Asn	Asp	Asn	Arg	Asp	Ala	Ala	Gln	Gly	Ala	Gln	Gly	Ser	Gln	Asp
	50					55					60				

Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly
 65 70 75 80
 Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly
 85 90 95
 Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly
 100 105 110
 Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
 115 120 125
 Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
 130 135 140
 Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
 145 150 155 160
 Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
 165 170 175
 Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
 180 185 190
 Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
 195 200 205
 His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
 210 215 220
 His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
 225 230 235 240
 Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Lys Lys
 245 250 255
 Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
 260 265 270
 Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
 275 280 285
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 290 295 300
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 305 310 315 320
 Pro Thr

<210> 65
 <211> 1527
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1504)
 <223> RXC02095

<400> 65

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Met Lys Thr Glu Gln
1 5

tcc caa aaq gca caa tta gcc cct aag aaa gca cct gaa aag cca caa 163
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln
10 15 20

agg atc cgg caa ctt att tcc gtg gag tgg cag cga cct tgg ctc acc 211
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr
25 30 35

tca ttc acc gta atc agc gct tta gct gca aag ttg ttt gaa ctt acc 219
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr
40 45 50

atc cct ctt ttg acc ggt ggt gct att gct atc gag ctc tga aat acc 307
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr
55 60 65

gga aat acc tta acc acc gac cta cta gac tgg ttc act tgg tgt gga 355
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly
70 75 80

tta agc gtg ttg acc agc gta att gca ctt atc gtg ctt ctc agc ttg 403
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu
85 90 95

ctc agc aat gcc agt caa ttc gga cgg cga tcc acc tca tgc aag ctc 451
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu
105 110 115

agc atg ggg gta cag cat gac gtc cgg ctt aaa acc atg agc tca ttg 499
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu
120 125 130

cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta 547
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val
135 140 145

gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gag 595
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala
150 155 160 165

atg ttg cgg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg 643
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu
170 175 180

gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg 691
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val
185 190 195

ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcc ctt 739
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu
200 205 210

ttt gag tta aag tgg tgg gct cag caa aag gct gag gat ctg acc aat 787

Pho	Ala	Ser	Thr	Trp	Ser	Ala	Gln	Gln	Lys	Ala	Ala	Asp	Leu	Thr	Thr		
215						220					225						
cat	gtg	gaa	gaa	act	gtc	acg	ggg	atc	agg	gtg	gtc	aag	gca	ttt	gcg	835	
His	Val	Glu	Glu	Thr	Val	Thr	Gly	Ile	Arg	Val	Val	Lys	Ala	Phe	Ala		
230					235				240					245			
cag	gaa	gac	ggc	gag	acc	gag	aaa	ttg	gat	ctc	acc	gca	cgt	gag	tta	983	
Gln	Glu	Asp	Arg	Glu	Thr	Asp	Lys	Leu	Asp	Leu	Thr	Ala	Arg	Glu	Leu		
				250				255						260			
ttt	goc	cag	ggc	atg	ggc	act	gca	agt	ctg	acg	gca	aag	ttc	atc	ccc	931	
Phe	Ala	Gln	Arg	Met	Arg	Thr	Ala	Arg	Leu	Thr	Ala	Lys	Phe	Ile	Pro		
				265				270					275				
atg	gtt	gag	cag	ctt	cag	cag	ctt	act	tig	gig	g'tc	aat	att	ctt	ggc	979	
Met	Val	Glu	Gln	Leu	Pro	Gln	Leu	Ala	Leu	Val	Val	Asn	Ile	Val	Gly		
	280					285						290					
ggg	ggg	tat	tig	ggc	atg	act	ggg	aat	atc	arg	g'g	g'g	act	ttt	ctg	1027	
Gly	Gly	Tyr	Leu	Ala	Met	Thr	Gly	His	Ile	Thr	Val	Gly	Thr	Phe	Val		
	295					300						305					
ggg	tat	tat	tac	tat	ctc	act	agg	tig	ttg	ggg	g'g	g'g	gct	agg	tcc	ctg	1075
Ala	Phe	Ser	Ser	Tyr	Leu	Thr	Ser	Leu	Ser	Ala	Val	Ala	Arg	Ser	Leu		
310					315					320					325		
ttg	ggg	atg	ctc	atg	agg	ttt	cag	tig	ggg	ctg	tat	tat	ctc	gag	ggc	1123	
Ser	Gly	Met	Leu	Met	Arg	Val	Gln	Leu	Ala	Leu	Ser	Ser	Val	Glu	Arg		
				330				335						340			
atc	ttt	gaa	gtc	att	gat	ctt	cag	act	gaa	ggc	acc	gat	cgt	gca	cac	1171	
Ile	Phe	Glu	Val	Ile	Asp	Leu	Gln	Pro	Glu	Arg	Thr	Asp	Pro	Ala	His		
				345				350					355				
ccc	ctg	tca	ctt	ccc	gac	act	ccc	ctg	ggt	ctg	tcc	ttc	aac	gac	gta	1219	
Pro	Leu	Ser	Leu	Pro	Asp	Thr	Pro	Leu	Gly	Leu	Ser	Phe	Asn	Asn	Val		
				360				365				370					
gat	ttc	cgt	ggg	att	ctc	aac	ggg	ttt	gag	ctg	ggg	gtt	cag	goc	ggg	1267	
Asp	Phe	Arg	Gly	Ile	Leu	Asn	Gly	Phe	Glu	Leu	Gly	Val	Gln	Ala	Gly		
				375			380				385						
gaa	acc	gtt	gtg	ttg	gtg	ggc	ccc	cca	ggt	tca	ggc	aag	acc	atg	gct	1315	
Glu	Thr	Val	Val	Leu	Val	Gly	Pro	Pro	Gly	Ser	Gly	Lys	Thr	Met	Ala		
				390		395			400					405			
gtg	cag	ctt	gct	gga	aac	ttt	tat	caa	cca	gac	agg	ggc	cac	atc	gcc	1363	
Val	Gln	Leu	Ala	Gly	Asn	Phe	Tyr	Gln	Pro	Asp	Ser	Gly	His	Ile	Ala		
				410				415						420			
ttt	gat	agg	aac	ggc	cat	ggc	act	ggc	ttc	gac	gac	ctc	acc	cac	agg	1411	
Phe	Asp	Ser	Asn	Gly	His	Arg	Thr	Arg	Phe	Asp	Asp	Leu	Thr	His	Ser		
				425				430					435				
gat	atc	ggc	agg	aat	ctc	atc	ggg	ggt	ttt	gat	gag	ccg	ttc	ttg	tac	1459	
Asp	Ile	Arg	Arg	Asn	Leu	Ile	Ala	Val	Phe	Asp	Glu	Pro	Phe	Leu	Tyr		
				440			445					450					
tcc	tcc	tcc	ata	ccg	cga	gaa	cat	ctc	gat	ggg	ttt	gga	tgt	cag		1504	
Ser	Ser	Ser	Ile	Pro	Arg	Glu	His	Leu	Asp	Gly	Phe	Gly	Cys	Gln			

455

460

465

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1527

<210> 66

<211> 468

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln
20 25 30

Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
65 70 75 80

Leu Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Ile Gly Arg Arg Tyr
100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
145 150 155 160

Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
165 170 175

Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
180 185 190

Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
195 200 205

Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
210 215 220

Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
225 230 235 240

Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
245 250 255

Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
260 265 270

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
 275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
 290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
 305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
 325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
 340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
 355 360 365

Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
 370 375 380

Gly Val His Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser
 385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr His Pro Asp
 405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
 420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp
 435 440 445

Gln Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly
 450 455 460

Phe Gly Cys Gln
 465

<210> 67
 <211> 295
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (84)..(272)
 <223> RXC03185

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 tcaactgaget gtcggaaacc acc atg aat gat ctt gca gct gaa ggt gaa aac 113
 Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
 1 5 10
 gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tat cgc ttc 161
 Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
 15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
 Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
 30 35 40

cag atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
 Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
 45 50 55

tca cgc gag tcc ctg taaaagcatt togtttttcg acg 295
 Ser Arg Glu Ser Leu
 60

<210> 68

<211> 63

<212> PRT

<213> Corynebacterium glutamicum

<220> 68

Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
 1 5 10 15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
 20 25 30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
 35 40 45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
 50 55 60

<210> 69

<211> 1170

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1147)

<223> RXA00115

<400> 69

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cgtatattgt gacctacacc ccatactgtt aggagtttcc atg ctc gac aat agt 115
 Met Leu Asp Asn Ser
 1 5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163
 Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly
 10 15 20

cgg ctc gaa ctc gaa gaa ggg ggt ctg att gag gat tgc tgg ttg gct 211
 Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala
 25 30 35

tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc 259
 Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu
 40 45 50

att cgg aag tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac	307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr	
55 60 65	
atc ggc aat gat cat ggc ctg gat cca tca aag tat ttc atc atc tcc	355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser	
70 75 80 85	
atc aac caa atc ggt aat ggt ttg tgg gtc tcc cct gac aac aag gct	403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala	
90 95 100	
gat gac agc atc tgg aag tcc aag ttc cgg aat gtt ggc att ggt gat	451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp	
105 110 115	
gat gtc gtt gcc cag gac ggg ctc ttg ggt gaa gac ttt ggt att acc	499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Gln Phe Gly Ile Thr	
120 125 130	
gag ttc ttt gtc gta gtt gat gtt tgg atg ggt ggt cag caa acc tat	547
Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr	
135 140 145	
gct tgg att gtt cgc ttc cat gat cca gtt cat cga gaa gct ggt atc	595
Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile	
150 155 160 165	
ggg ggc aat ggg aag aac act cct cat gat ttc atc ttc tcc cag act	643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr	
170 175 180	
ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac	691
Ile Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Gln Tyr	
185 190 195	
tcc ttc cat gaa gag gta gat gat gga ctt cgg cgt caa tgg cat ctt	739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu	
200 205 210	
tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg	787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp	
215 220 225	
cgt cgc ctg gga ctt gaa agt aag gag tca gtc ctc gcg gac ttc ctg	835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu	
230 235 240 245	
gat cgg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct	883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala	
250 255 260	
tgg aag tgg cag cat ggc gat gtc tct cgc cac aac ggc ggc gac ttg	931
Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu	
265 270 275	
gca gcy gct ctt ggc gga gtc aag gct aag acc ttc gtt atg ccc atc	979
Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile	
280 285 290	

agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa gaa gca 1027
 Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
 295 300 305
 ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac 1075
 Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
 310 315 320 325
 ctt ggg ctt ttt aac gtc tct gag aat tac atc cca aat atc gac aaa 1123
 Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
 330 335 340
 aat ctg aaa gag ctg ttc gag agc caaacactga tgcacagag cct 1173
 Asn Leu Lys Glu Leu Phe Glu Ser
 345

<210> 20

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<430> 70

Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Glu Gly Pro Tyr Glu
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Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu
 20 25 30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
 35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
 50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
 65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
 85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
 100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
 115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly
 130 135 140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His
 145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe
 165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe
 180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg
 195 200 205

Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp
 210 215 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val
 225 230 235 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr
 245 250 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His
 260 265 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr
 275 280 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys
 290 295 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Asn Val Ile Glu
 305 310 315 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile
 325 330 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser
 340 345

<210> 71

<211> 1291

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (131)..(1231)

<223> RXN00403

<400> 71

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aagttttagt ctgttcacac cagaacaggc ggttatcttc atg ccc acc ctc gcg 115
 Met Pro Thr Leu Ala
 1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
 Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
 10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211
 Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
 25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
 40 45 50

aac gac tcc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
 55 60 65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt	355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys	
70 75 80 85	
acc aac gtc atc ggt ggt tgc aac ggt tcc aac gga cct ggc tcc atg	403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met	
90 95 100	
cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc aag tcc att	451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile	
105 110 115	
ogt cat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc	499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile	
120 125 130	
acc aag gtc ccc cca gta att ggt ggt tcc atg ggt ggt ggt ggt aac	547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr	
135 140 145	
cta gag tgg ttc gga arg tac cta gaa aat ttc ggc gca ggt atc ggt	595
Leu Glu Trp Ala Ala Met Tyr Pro Gln Thr Val Gly Ala Ala Ala Val	
150 155 160 165	
cta gca att tct gca cag ccc aac gcc tgc aac atc ggc att cca tcc	643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser	
170 175 180	
ccc cca att aag ggc att gaa aac gat cag tac tgg tac gaa ggc aac	691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Gln Gly Asn	
185 190 195	
tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc gga	739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg	
200 205 210	
ggc atc gcc cag ctc aac tac cgt ggc gaa cta gaa atc gac gaa cgc	787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg	
215 220 225	
ttc ggc acc aaa gcc cca aag aac gaa aac cca ctc ggt ccc tac cgc	835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg	
230 235 240 245	
aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac cca gca	883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala	
250 255 260	
gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc	931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr	
265 270 275	
gac gcc ctc aac cgc cag gac att ggt cgc gac cgc gga ggc ctc aac	979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn	
280 285 290	
aag gca ctc gaa tcc atc aaa gtt cca gtc att gtc gca ggc gta gat	1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp	
295 300 305	

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat ggt ttv ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ttc ttc agc ctc atc tcc cca gag gaa gag aac cct tgg acc tac atc 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
 360 365 370

gag ttc tac atc taataggcat ttacgacaaa ta; 1214
 Glu Phe Tyr Ile
 375

<210> 72

<211> 371

<212> PRP

<213> Corynebacterium glutamicum

<100> 72

Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
 145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
 165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His

180

185

190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Gln Ser Tyr
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335

Ser Ile Val Gly His Asp Ala Phe Leu Thr Gln Ser Arg Gln Met Asp
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
370 375

<210> 73

<211> 1210

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1210)

<223> FRXA00403

<400> 73

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aagtttttagt cttgtccacc cagaaacaggc ggtttttttc atg jcc acc ctc ggc 115
Met Pro Thr Leu Ala
1 5

cct tca ggt caa att gaa atc caa ggc atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
10 15 20

gac ppa gaa atc att aca aac gat gaa atc gac tat caa cgc tgg ggt 211

Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
 25 30 35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa 259
 Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
 40 45 50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg 307
 His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
 55 60 65

ctc ggt ccc gcc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
 Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
 70 75 80 85

acc aac gtc atc ggc ggt tgc aac ggt tcc aac gga cct ggc tcc atg 403
 Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
 90 95 100

cat cca gat gga aac tcc tgg gct aac cgc ttc ccc gcc acg tcc att 451
 His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
 105 110 115

cgt gat cag gta aac gcc gaa aac cca ttc ctc gac gca ctc gcc atc 499
 Arg Asp Gln Val Asn Ala Gln Lys Gln Phe Leu Asp Ala Leu Gly Ile
 120 125 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
 Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
 135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt gcc cca gct gct gtt 595
 Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Val
 150 155 160 165

ctt gca gtt tct gca cgc gcc agc gcc tgg aac atc gcc att cca tcc 643
 Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
 170 175 180

gcc caa att aag ggc att gaa aac gac cac cac tgg cac gaa gcc aac 691
 Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
 185 190 195

tac tac gaa ttc ggc tgc aac cca ccc acc gga ctc gcc gcc gcc cga 739
 Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
 200 205 210

cgc atc gcc cac ctc acc tac cgt gcc gaa cta gaa atc gac gaa cgc 787
 Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
 215 220 225

ttc gcc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
 Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
 230 235 240 245

aag ccc gac cag cgc ttc gcc gtc gaa tcc tac ttg gac tac caa gca 883
 Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
 250 255 260

gac aag cta gta cag cgt ttc gac gcc gcc tcc tac gtc ttg ctc acc 931
 Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr

265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
 Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
 280 285 290

aag gca ctc gaa tac atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
 Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
 295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
 Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
 310 315 320 325

ctg gga aat cta ctg gca atg gca aat atc gta tcc cct ctc ggc cac 1123
 Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
 330 335 340

gat ggt ttc ctt aac gaa agc cgt caa atg gat cgc atc ctg aga aac 1171
 Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
 345 350 355

ctc ttc agc ccc atc ttc cca gac gac gat aac att tgg 1219
 Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
 360 365 370

<210> 74
 <211> 300
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 74
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Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
 20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
 35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
 50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
 65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
 85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
 100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
 115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
 130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val

145

150

155

160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
355 360 365

His Ser
370

0110075

0110087

0110094

0110094 Corynebacterium glutamicum

0120000

0120000

0120000 (101)..(664)

0120000 RX303158

0400075

caaaagctcac cgaaggcaac aacgccaagt tgggtgttga caaacaccttg gcaccccat 60

acctgcagca gccactaaaa ctgggcgcac acgcaagtcc ttg cac tcc acc acc 115
Leu His Ser Thr Thr

1

5

aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
 Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
 10 15 20
 aac gac cag gaa atg gac gaa gaa cag cag ttc atg cag ggc ggc atc 211
 Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
 25 30 35
 gga cag atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
 Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
 40 45 50
 aag acc ctt gca gtc cgc atg gat cgc cac tgc gac aac gca gaa aag 307
 Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
 55 60 65
 atc gca gaa ttc cag gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
 Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
 70 75 80
 cca ggt cag aag aac cac cca ggc cac gaa gtc gca ggc aag cag atg 403
 Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
 85 90 95
 aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
 Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
 105 110 115
 gca cct aag aag ttc tgt acc tcc acc aac ctg atc tgt ctg gcc gag 499
 Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
 120 125 130
 ttc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
 Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
 135 140 145
 ctc cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595
 His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val
 150 155 160
 cgc acc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
 Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
 170 175 180
 gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
 Glu Gln Ala Leu Asn Asn Leu
 185

10100-76

1110-188

1120-PST

1113-Corynebacterium glutamicum

10100-76

Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly
 5 10 15

Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe
 20 25 30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu
35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val
145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
165 170 175

Ile Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu
180 185

<210> 77

<211> 617

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(594)

<223> FRXA60254

<400> 77

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Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
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tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
20 25 30

gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144
Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
35 40 45

ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag 192
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
50 55 60

acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile

80

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
100 105 110

Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
115 120 125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
130 135 140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
145 150 155 160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
165 170 175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
180 185 190

Gln Ala Leu Asn Asn Leu
195

<210> 79

<211> 170

<212> DNA

<213> Corynebacterium glutamicum.

<220>

<221> CDS

<222> [101]...[1147]

<223> EXA02032

<400> 79

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tgtgcaagcg ggacggcag ccagaactcc tgggtgagac atg aac cca cct atc 115
Met Asn Pro Pro Ile
1 5

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc 163
Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg
10 15 20

gat ggc aat gat gga tgg ggt gca ttc gag gct gcc atg gga act cta 211
Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu
25 30 35

gat ggt ggg ttc ggc gta tct tat tct tca ggt ttg gca ggc gca acg 259
Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr
40 45 50

tcg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa 307
Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys
55 60 65

gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc 355
Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg
70 75 80 85

gga agg ctg aac gtt cga act gtt gat gca gac aat acc gaa gaa gtc 403
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val
90 95 100

att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tgg atc gct 451
 Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala
 105 110 115

aat cgg acg arg gtg gta gct gat atc cct gca ata gtc gac ggt gtg 499
 Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val
 120 125 130

cgt ggg ctt gga gtt ttg act gtc gtt gac gga aat ttc cca aag cca 547
 Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro
 135 140 145

att cgt caa cgt cca ttg gaa ctt ggt gct gat att gtg ctt tac tgg 595
 Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr Ser
 150 155 160 165

gca acc aaa ctt atc ggt gga cct tct gat ctt ctt ctt aga gtc gca 643
 Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala
 170 175 180

gta ttc aat ttt gag caa car ggt tgg ttt ctt gtt aat tag gtt gat 691
 Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg His
 185 190 195

gat cat ggt tgg gtg cgg gga ggt ctt gaa gag ttt ctt gct ctc cgt 739
 Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala Phe Leu Ala Leu Arg
 200 205 210

gga ttg tat tcc ttg cgg gtc cgt ctt gat aga gaa gaa tcc aat gta 787
 Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala
 215 220 225

gca aaa ctt tcc ctt gga ctt aat ggt gat cct tcc gtt aac agt gta 835
 Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val
 230 235 240 245

aat tat cca gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg cga 883
 Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg
 250 255 260

gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca 931
 Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala
 265 270 275

acc cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc 979
 Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr
 280 285 290

cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc 1027
 His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr
 295 300 305

agg cgg gat gct gaa gtg gtg gca gaa gta cgg atg act ctt tgc cgc 1075
 Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg
 310 315 320 325

gtr tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac 1123
 Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn
 330 335 340

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Ala Ser Ile Asp Lys Val Leu Gly
345

<210> 80

<211> 349

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

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Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala
20 25 30

Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly
35 40 45

Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr
50 55 60

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
65 70 75 80

Arg Met Glu Ala Arg Gly Arg Lys Lys Val Arg Thr Val Asp Ala Asp
85 90 95

Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp
100 105 110

Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
115 120 125

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
130 135 140

Phe Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp
145 150 155 160

Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
165 170 175

Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu
180 185 190

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
195 200 205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
210 215 220

Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
225 230 235 240

Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
245 250 255

Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
260 265 270

Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
 275 280 285

Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
 290 295 300

Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
 305 310 315 320

Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu
 325 330 335

Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
 340 345

<210> A1
 <211> 861
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(838)
 <223> RM38154

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 1 5
 aac acc gag ggt ttc tcc act gca tgg att caa ggt ggg tat gag cca 163
 Asn Thr Glu Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20
 gac gac tac tac ggt tgg att aac acc cca atc tat gac tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35
 ttc gcg cag aac ggt cca aac gaa ctg cgc aaa ggc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50
 cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65
 ctg gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg ggt gca 355
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
 70 75 80 85
 acc gac atc ctg ttc cgc atc atc ctg aag cgc ggc gat cag atc gtc 403
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
 90 95 100
 ctg ggc aac gat ggt tac ggc gga acc tac cgc ctg atc gac acc gta 451
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
 105 110 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtc 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
120 125 130

gaa gag gtc aag gca ggc atc aag gaa aac aac aag ctg atc tgg gtc 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
135 140 145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
150 155 160 165

gaa aag ctg acc gaa ggc acc aac gcc aag tgg gtt gtt gaa aac acc 643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
170 175 180

tgg gca tcc cca tac atg cag cag cca ata aac ctg ggc gca cac gca 691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
185 190 195

agt cct tgg act cca gca cca agt aca tgg aag gaa act tgg aag tgg 739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu
200 205 210

tgg aag gaa tgg tgg gca cca aag gcc aag aac tgg aag aag aag tgg 787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys
215 220 225

tgt tca tgc agg ggc gca tcc gac cga acc cat cag ttt tgg atg cat 835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His
230 235 240 245

acc tgaacaggg tggat aag aac 881
Thr

<310> 32
<311> 246
<312> PRT
<313> Corynebacterium glutamicum

<400> 32
Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
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20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
65 70 75 80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
85 90 95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140

Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr
 145 150 155 160

Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu
 165 170 175

Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys
 180 185 190

Leu Gly Ala His Ala Ser Pro Cys Thr Pro Ile Pro Ser Thr Ser Lys
 195 200 205

Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys
 210 215 220

Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His
 225 230 235 240

Gln Phe Ser Met His Thr
 245

<210> 83
 <211> 703
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(703)
 <223> FRXA02768

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 <223> All occurrences of n = any nucleotide

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 Leu Ser Phe Asp Pro
 1 5

aac acc cag ggt ttc tcc act gca tcc att cac gct ggg tat gag cca 163
 Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
 10 15 20

gac gac tac tac ggt tcc att aac acc cca atc tat gcc tcc acc acc 211
 Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
 25 30 35

ttc ggc cag aac gct cca aac gaa ctg cgc aaa agc tac gag tac acc 259
 Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
 40 45 50
 cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca 307
 Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
 55 60 65
 ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca 355
 Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
 70 75 80 85
 acc gac atc ctg ttc cgc atc atc ctc aag cgc ggc gat cgc atc gtc 403
 Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
 90 95 100
 ctc ggc aac gat gct tac agc gca ttc tac cgc ctg ttc gac acc gta 451
 Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
 105 110 115
 ttc acc gca tgg cgc gtc aac tac aac ttt ttt ttt ttc tac ttc ctg 499
 Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
 120 125 130
 gaa gat gtr aac gca ggc atc aag gac ttc ttc aag gtc gat ttt gtt 547
 Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
 135 140 145
 gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca 595
 Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
 150 155 160 165
 gtn tgc aaa act tca ccc gaa agg cac aaa acc aaa gat tgt tgt ttg 643
 Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
 170 175 180
 aca aca cct tgg cat tcc cca tac ctg aag aan aca ctc aaa ant tnn 691
 Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
 185 190 195
 yng aac aag gag 703
 Xaa His Thr Gln
 200

<210> 84

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<20>

<23> All occurrences of Xaa = any amino acid

<400> 84

Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
 1 5 10 15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
 20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
 35 40 45
 Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
 50 55 60
 Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65 70 75 80
 Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
 85 90 95
 Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
 100 105 110
 Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
 115 120 125
 Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
 130 135 140
 Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu
 145 150 155 160
 Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
 165 170 175
 Gln Ala Tyr Tyr Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Val Xaa
 180 185 190
 Pro Leu Lys Xaa Xaa Xaa His Thr Gln
 195 200

<210> 85
 <211> 1113
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1090)
 <223> RXA00216

<400> 85
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 ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt 115
 Leu Gly Ala Tyr Gly
 1 5
 tta ggt gag att cct gga aaa tcc gcc ggc gaa gcc gcc gac att att 163
 Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
 10 15 20
 cag ggt gaa acg ggc gat att ctc cat att cct cag att ccg ggc cga 211
 Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
 25 30 35
 ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
 Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met

40	45	50	
atc aac gtt gat cgc ggg gcc cga tat tgg gtg atg agc aca cgc ccc	307		
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro			
55 60 65			
agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat	355		
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp			
70 75 80 85			
ggg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa	403		
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln			
90 95 100			
gtt gct ggt ccc tgg acg tta ggt ggg cgc att gag ttg gcc act ggc	451		
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly			
105 110 115			
cat cgc ggt ttg tat gat cgc ggt gag atg cgt gat ctg acg tag gag	499		
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala			
120 125 130			
ctg atc ggc ggc atc gat ggc cat ggc cgc aag gtt gct tgg cga ttt	547		
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe			
135 140 145			
ggg atc gaa gta tgg tta caa atc tat gat tag tgg cta aca tct att	595		
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu			
150 155 160 165			
atc aac ggt tat ctg act ggc act taa acc att gac att att att tgg	643		
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala			
170 175 180			
gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tgg	691		
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser			
185 190 195			
att gag ggt cag aca tat ctg aac ctg acc ggc cag att cct act tgg	739		
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp			
200 205 210			
gat gtg gct cgg ggt ggc ggc gcc gat act gtg cag att tcc atg gat	787		
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp			
215 220 225			
caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc	835		
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr			
230 235 240 245			
agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta	883		
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val			
250 255 260			
gat gaa ctg ctg gag cga cgg cgg caa aag gcc gtt gag gta gca cgc	931		
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg			
265 270 275			
ttt ttt gat agt tta ggt gtg ggc cga aac tat ctg gtg gat gct gtt	979		
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val			
280 285 290			

gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc 1027
 Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
 295 300 305

ggg cag ggt tat cgc atg gcc cgg gtg atg tgg gag atg ttg tgg aag 1075
 Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
 310 315 320 325

gat tca tgc gac att taaggcttta cggggcggg gat 1113
 Asp Ser Cys Asp Leu
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<213> 86

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
 1 5 10 15

Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
 20 25 30

Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
 35 40 45

Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
 50 55 60

Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65 70 75 80

Asp Met Asp Leu Asp Ala Cys Gln Gln Thr Trp Gly Thr Gly Val Asp
 85 90 95

Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
 100 105 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
 115 120 125

Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
 130 135 140

Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
 145 150 155 160

Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
 165 170 175

Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
 180 185 190

Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
 195 200 205

Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
 210 215 220

Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
225 230 235 240

Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
245 250 255

Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
260 265 270

Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
275 280 285

Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
290 295 300

Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
305 310 315 320

Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
325 330

<210> 87

<211> 551

<212> DNA

<213> Corynebacterium glutamicum

<217>

<221> CDS

<222> (1)...(528)

<223> RXA02197

<400> 87

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Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
1 5 10 15

ttg tgc atc gag gat ttc att cgc cca cgc gag caa gct gtc aag gac 96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
20 25 30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
35 40 45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
50 55 60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc 240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
65 70 75 80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
85 90 95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
100 105 110

ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tat tgc cct 384
 Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt 432
 Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

ctc ggc gtg gag ttg tac gag gaa ctc cag atg ctc cca gag cag tcc 480
 Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

aca gac ggc ttt gtg ctc tac cac cca gag gca aat tac ttt aac gtc 528
 Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

taaacacat gaaaggaat act 551

<10> ++
 <11> 176
 <12> FRT
 <13> Corynebacterium glutamicum

<400> 88
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 1 5 10 15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
 20 25 30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
 35 40 45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
 50 55 60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65 70 75 80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
 85 90 95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
 100 105 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
 115 120 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
 130 135 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
 145 150 155 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
 165 170 175

<210> 89

<211> 2599
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)...(2599)
 <223> RXN02198

<400> 89
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 agttggggaa ttgtataate cgtactango tgtctacaca atg tct aat tca gtt 115
 Met Ser Thr Ser Val
 1 5
 act tca cca gtt aac aac aac gaa cat tcc tcc aca ttt ttg cat ggg 163
 Thr Ser Ile Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
 10 15 20
 ttg gaa aac cat ttg ttg atc ggg gac ggc aac atg gac aac cag ttc 211
 Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr His Leu
 25 30 35
 aaa ggg ttt gat ctg gac gtg aca aac gat ttc att gat cca gag ggg 259
 His Gly Ile Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Ala Gly
 40 45 50
 agt att gat att atc aac gac aac ggg ggc gat ttg ttt agt cag att 307
 Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Glu Ile
 55 60 65
 aac gat gtt tat ttt gag ggg gga ggt aac ttg gtt gat aac aat aat 355
 His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70 75 80 85
 ttt ggt tgc aac ctg cgg aac ttg ggg gat tat gac atc gat gat agt 403
 Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
 90 95 100
 tgc agt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct 451
 Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala
 105 110 115
 gat gag atg ggg cgg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt 499
 Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly
 120 125 130
 tcc ctg gga cct gga acg aag ctt cca tcc ctg ggc cat gca cgg tat 547
 Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr
 135 140 145
 gca gat ttg cgt ggg cac tac aag gaa gca ggc ctt ggc atc atc gac 595
 Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp
 150 155 160 165
 ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag 643
 Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Glu Asp Leu Leu Glu
 170 175 180
 gtc aag gct gag gtt cac ggc gtt caa gat gcc atg gat gaa ttt gat 691

Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aaa ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
200 205 210	
atg ctc atg gct tct gag atc ggt gcc agc ttg aaa gag ctg cag cca	747
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg agt tac ctg tcc aag cac gcc gat att ctt gtc	853
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
ctg ctg atg cct aac gca ggt ctt cct ctc ctg ggt aaa aac gct cca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
gaa tac cca ctt gag gct gag gat ttg agc gag gcc atg tct gaa ttc	949
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Ile	
280 285 290	
gtc tcc aac tat gcc ctg tcc agc gta gct agt agt agt gcc aac aaa	1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
act gag cac aac agt agc gta tgc gat agc ctg gta ggt gtt cta gag	1087
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
310 315 320 325	
cag gaa acc tcc aca ctg acc aag atc cct gca gcc cct gtt gag cag	1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
330 335 340	
gcc tcc gcc gag gtg gag aaa gag gac tcc gtc gcc tgc ctg tac acc	1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	
345 350 355	
tgc gtg cca ttg tcc cag gaa acc gcc att tcc atg atc ggt gag cgc	1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
360 365 370	
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc	1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
375 380 385	
gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt	1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	
390 395 400 405	
gca cac atg ctg gat ctt tgt gtc gat tac gtg gga cga gac gcc acc	1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	
410 415 420	
gcc gat atg gcc acc ttg gca gca ctt ctt gct acc aga tcc act ttg	1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	

425	430	435	
cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt	1459		
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu			
440	445	450	
gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac	1507		
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp			
455	460	465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555		
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys			
470	475	480	485
cag cac ggt gag gcc ggg gtt ggg ctg acc att gat gag gaa ggc cag	1603		
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln			
490	495	500	
aca cgt aac ggt gag cac aag gtg cgc att gct aaa cga ctg att gat	1651		
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp			
505	510	515	
gat atc aac ggt agc tac ggc ctg gat atc aaa gac atc gtt gtg gac	1699		
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp			
520	525	530	
tac atg att ttt cca atc tct act agc ttt gaa cca aac att cga gat	1747		
Lys Leu Thr Phe Pro Ile Ser Thr Gly Gln Gln Glu Thr Arg Arg Asp			
535	540	545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aac ctg tac cca	1795		
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro			
550	555	560	565
gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac	1843		
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn			
570	575	580	
cct gct gaa cgc cag gtt ctt aac tct gtg ttc ctg aat gag tgc att	1891		
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile			
585	590	595	
gag gct ggt ctg cac tct gcg att gcg cac agc tcc aag att ttg ccg	1939		
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro			
600	605	610	
atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc	1987		
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val			
615	620	625	
tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag	2035		
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln			
630	635	640	645
ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa	2083		
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu			
650	655	660	
cag ctg gcc gct atg cct ttg ttt gag cgt ttg gaa cag cgc atc atc	2131		
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile			
665	670	675	

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gga ggc atg aag 2179
 Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
 680 685 690

gag aag tct cct att ggc atc atc aac gag gac ctt ctc aac ggc atg 2227
 Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
 695 700 705

aag aac gtg ggt gag atg ttt ggt tcc gga gag atg gag ctg gaa ttc 2275
 Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
 710 715 720 725

gtg ctg caa tcc gca gaa acc atg aaa act ggc gtg ggc tat ttc gaa 2323
 Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
 730 735 740

tct ttc atg gaa gag gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa 2371
 Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

ggt aag ggc aaa atc gtc gtg ggc acc gtc aag ggt gac ggt gac gat 2419
 Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
 760 765 770

tct ggt aag aac ttc gtg gac atc atc atc atc atc atc atc atc atc 2467
 Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
 775 780 785

gtg gtg aac ttc ggc atc aag cag gca ctg tcc ggc atg ttc gaa gca 2515
 Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
 790 795 800 805

gtg gaa gaa aac aac gaa gac gtc atc ggc atc ttc gga ctt ctt gtg 2563
 Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
 810 815 820

aag tcc acc gtg gtg atg aag caa acc atc agc gac 2599
 Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp
 825 830

<210> 90

<211> 833

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Met Ser Thr Ser Val Thr Ser Pro Ala His Asn Asn Ala His Ser Ser
 1 5 10 15

Glu Phe Leu Asp Ala Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala
 20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
 35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu

65	70	75	80
Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr	85	90	95
Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val	100	105	110
Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg	115	120	125
Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu	130	135	140
Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala	145	150	155
Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala	165	170	175
Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala	180	185	190
Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val	195	200	205
Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu	215	220	225
Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala	230	235	240
Thr Gly Pro Asp Glu Met Ser Gln His Leu Arg Tyr Leu Ser Lys His	245	250	255
Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu	260	265	270
Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln	275	280	285
Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly	290	295	300
Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val	305	310	315
Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala	325	330	335
Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val	340	345	350
Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser	355	360	365
Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu	370	375	380
Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln	385	390	395
			400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Ile Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
 610 615 620
 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
 625 630 635 640
 Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
 645 650 655
 Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
 660 665 670
 Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
 675 680 685
 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
 690 695 700
 Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
 705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Gln Glu Glu Ala Glu Ala Thr Gly
740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
785 790 795 800

Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met
805 810 815

Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser
820 825 830

Asp

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<223> FRXA02195

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Met Ser Thr Ser Val
1 5
act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat ggc 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20
ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
25 30 35
caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
40 45 50
tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
55 60 65
cac cgc gcc tac ttt gag ggc gga ggt gac ttg gtt gag aat aat act 355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt	403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
90 95 100	
tgc cgt gag ctt gcc tac aag ggc act gca gtc gct agg gaa gtc gct	451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
105 110 115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtc gtt ggt	499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
120 125 130	
ttc ctg gga cct gga acg aag ctt cca tgc ctg ggc cat gca cag tat	547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
135 140 145	
gca gat ttg cgt ggg cac tac aag gaa gca gtc att ggc atc att gac	595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	
150 155 160 165	
ggt cgt agg gat ggc ttt tgc att gat act gct cag gac ttg att cag	643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
170 175 180	
ttc aac cct agc gtt cac agc gtt cca gat gca att gct aac att gat	691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aaa ttc ttg acc att att tgc cag gtc acc gta gag acc acc gtc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
200 205 210	
atg ctc atg ggt tct gag atc ggt gct ggc ttg aca ggc ctg cag cct	787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
215 220 225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag	835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
230 235 240 245	
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtc	883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
250 255 260	
tgc gtc atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
gaa tac cca ctt gag gct gag gat ttg ggc cag ggc ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
280 285 290	
gtc tcc gaa tat ggc ctg tcc atg gtc ggt ggt tgt tgt ggc acc aca	1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
cct gag cac atc cgt ggc gtc ccg gat ggc gtc gtt ggt gtt cca gag	1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
310 315 320 325	

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Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln	
330 335 340	
gac tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tgg ctg tac acc	1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr	
345 350 355	
tgg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc	1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg	
360 365 370	
acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc	1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly	
375 380 385	
gat tgg gaa aag tgt gtg gat att qcc aag cag caa acc cgc gat ggt	1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly	
390 395 400 405	
gaa caa atg ttg ggt ctg tgg gtg gat taa gtc gga gga gac ggt aac	1361
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr	
410 415 420	
gac gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg	1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu	
425 430 435	
gaa atc atg att gac tcc aca gag aca gat gtt att tgc aca ggc att	1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Gln Val Ile Arg Thr Gly Leu	
440 445 450	
gag caa ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac	1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp	
455 460 465	
ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag	1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys	
470 475 480 485	
cag caa ggt gcg gac gtg gtt gcg ctg acc att gat gag gaa ggc cag	1603
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln	
490 495 500	
gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac	1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp	
505 510 515	
gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac	1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp	
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Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp	
535 540 545	
ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctg tac caa	1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro	
550 555 560 565	
gaa atc gac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac	1843

Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn	
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cct gct gca cgc cag gtt ctt aac ttt gtg ttc ctc aat gag tgc att	1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile	
585	590 595
gag gct ggt ctg gac tct ggc att gag cac agc tcc aag att ttg cgc	1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro	
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atg aac cgc att gat gat cgc cag cgc gaa gtg ggc ttg gat atg gtc	1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val	
615	620 625
tat gat cgc cgc aac gag gat tac gat ccc ctg cag gaa tcc atg cag	2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln	
630	635 640 645
ctg ttt gag ttc gtt tct gat gcc gat ggc aag gat gct ttc att gaa	2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu	
650	655 660
gat ctg gca ttc atg att ttg ttt gat cgt ttg gaa cac ttc atg atc	2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile	
665	670 675
atg ggt gat aag aat ggc att gag gat gat ttg tta gca ppc att aag	2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys	
680	685 690
gag aag tct cct att gag atc atc aac gag gac ctt ctc aac ggc atg	2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met	
695	700 705
aag acc gtg gat gag ctg ttt ggt tcc gga cag atg cag ctg ccc ttc	2275
Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe	
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gtg ctg caa tcc gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa	2323
Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu	
730	735 740
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Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu	
745	750 755
ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat	2419
Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp	
760	765 770
atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac	2467
Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp	
775	780 785
gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca	2515
Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala	
790	795 800 805
ggc gaa gaa cac aaa gca gac gtc atc ggc atg tcc gga ctt ctt gtg	2563
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810

815

820

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2578

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Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
35 40 45
Leu Asp Leu Val Gly Cys Asn Gln Ile Leu Asn Asp Thr Arg Pro Asp
50 55 60
Val Leu Arg Gln Ile His Arg Ala Tyr Phe Gln Ala Gly Ala Asp Leu
65 70 75
Val Gln Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
85 90 95
Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
100 105 110
Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
115 120 125
Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
130 135 140
Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
145 150 155 160
Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
165 170 175
Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
180 185 190
Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
195 200 205
Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
210 215 220
Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
225 230 235 240
Thr Gly Pro Asp Gln Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
245 250 255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
 260 265 270
 Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
 275 280 285
 Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
 290 295 300
 Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
 305 310 315 320
 Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
 325 330 335
 Gly Phe Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
 340 345 350
 Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
 355 360 365
 Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
 370 375 380
 Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
 385 390 395 400
 Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe

530

535

590

Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
595 600 605

Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
610 615 620

Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
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Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
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Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
660 665 670

Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
675 680 685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
690 695 700

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
785 790 795 800

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805 810 815

Ser Gly Leu Leu Val Lys Ser Thr Val Val
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<217> EXN03074

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 Met Thr Gln Ser Ala
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cca gaa ttc att gcc acc gca gac ctg gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
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gag gaa tca tgc gac act cag ttt cca aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

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 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

atg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg atg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cag aac ggt cta gta ggt gac atc att gaa 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att gga gat tcc gca ctg atc ggc aac atc aac ttt ggt ttt aac ggt 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cca 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gta gta tcc att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
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Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
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 Met Thr Gln Ser Ala
 1 5

caa gaa ttc att gcc acc gca gac ctg gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
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ggc caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctg 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

atg aaa tcc atc ctg agc gag gat aat cct ggg gga gtc atg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gag cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gac 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac cgg cgg aaa tcc act aaa act ggt acc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

gac gta gta gta tgg att ggt ggc act gac ttc att act ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

acc tcc gta gta tcc gac gga att att gta att gac tgg cta att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

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 Gln

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<211> 160

<212> FRT

<213> Corynebacterium glutamicum

<400> 96

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 35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

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 Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg
 135 140 145

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Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn	
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gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt	643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu	
170 175 180	
gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt	691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly	
185 190 195	
gtc acc gag gaa acc acc acc ggt gtc cac cgc ctg tac cac ttc gct	739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala	
200 205 210	
gaa gaa ggt ggt ctg act ttc gca gag atg aac gtc aac gac gct gtc	787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val	
215 220 225	
act aat ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile	
230 235 240 245	
gac ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val	
250 255 260	
act ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	931
Leu Val Lys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe	
265 270 275	
acc ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt ggt	979
Asp Gly Glu Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn	
280 285 290	
gct att gag gct gag atg gat ggc tac tct ggc gtc acc gtt gat gag	1027
Ala Leu Glu Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu	
295 300 305	
gcc atc gag gac gcc gac atc gtg atc acc ggc acc ggc aac aag gac	1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp	
310 315 320 325	
atc att tcc ttc gag cag atg ctg aag atg aag gat cac gct ctg ctg	1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu	
330 335 340	
ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg	1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu	
345 350 355	
cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag	1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu	
360 365 370	
ttc acc ttc tcc gac ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc	1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg	
375 380 385	
ctg ttg act ctt ggc aat gcc acc gga cac cca tca ttt gtc atg tcc	1315

Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac 1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac 1411
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp
425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggt ggt cag ctc acc 1459
Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc 1507
Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
455 460 465

cca ttc aag ccg gag cac tac cgc tac taataatg taataatg ggc 1557
Pro Phe Lys Pro Glu His Tyr Arg Tyr
470 475

<213> 9A

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 99

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20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ile Val Val Gly Ser
85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
145 150 155 160

Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met

165	170	175
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala 180 185 190		
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg 195 200 205		
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn 210 215 220		
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr 225 230 235 240		
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met 245 250 255		
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly 260 265 270		
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu 275 280 285		
Ala Asp Pro Ile Asn Ala Leu Ile Ala Ile Met Asp Gly Tyr Ser Val 290 295 300		
Val Thr Val Asp Glu Ala Ile Glu Arg Ala Asp Ile Val Ile Thr Ala 305 310 315 320		
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys 325 330 335		
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp 340 345 350		
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys 355 360 365		
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val 370 375 380		
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro 385 390 395 400		
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile 405 410 415		
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu 420 425 430		
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu 435 440 445		
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly 450 455 460		
Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr 465 470 475		

<211> 128
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 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(105)
 <223> FRXA00132

<400> 93
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 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
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 att aag tac atc gcc gat gac gtt gga gcc cca ttc aag cag gag tac 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30
 tac cgc tac taatgattgt cagcattgag gga 128
 Tyr Arg Tyr
 35

<211> 100
 <212> 35
 <213> PRT
 <213> Corynebacterium glutamicum

<400> 100
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30
 Tyr Arg Tyr
 35

<210> 101
 <211> 1396
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1396)
 <223> FRXA01371

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 ttctctaatt ttcatcttct taaaaggagc tgcgcaggac atg gca cag gtt atg 115
 Met Ala Gln Val Met
 1 5
 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
 10 15 20
 att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cga aag 211

Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys		
			25					30					35				
gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggg	tct	259	
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser		
		40					45					50					
atc	caa	atg	aag	gtc	cag	acc	ggc	gtg	ctt	att	gag	aag	ctc	aac	gct	307	
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala		
	55					60					65						
ttg	ggc	gct	gag	gtt	cct	tgg	gct	tcc	tgc	aac	att	ttc	tcc	acc	cag	355	
Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln		
	70				75					80				85			
gat	gag	gct	gca	ggg	gat	atc	gtt	gtc	ggc	tcc	ggc	aag	gtc	gaa	gag	403	
Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu		
			90					95					100				
cca	gtt	gtt	ggt	aca	ala	ttc	ggg	tgg	aag	ggt	gag	tcc	gtg	gag	gag	451	
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu		
			105					110					115				
tac	tgg	tgg	tgc	atc	aac	cag	atc	ttc	agg	tgg	ggc	gct	ggt	ctg	cca	499	
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro		
	120					125					130						
aac	att	att	ctc	gac	gac	ggc	ggg	gat	gtt	aac	atg	ggt	gtt	att	ggt	547	
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg		
	135					140					145						
ggg	gat	gat	tac	gag	cag	gct	ggg	ctg	gtt	cca	cca	gca	gag	gtc	aac	595	
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn		
	150				155					160				165			
gat	tcc	gat	gag	tac	atc	gca	ttc	tgg	ggc	atg	ctg	ggg	gag	gtt	ctt	643	
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu		
			170					175					180				
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	ggc	gtt	aag	ggg	691	
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly		
		185						190					195				
gtc	acc	gag	gaa	acc	acc	acc	ggg	gtg	cac	ggc	ctg	tac	gac	ttc	gct	739	
Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala		
		200					205					210					
gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	ggg	atg	aac	gtc	aac	gac	gct	gtc	787	
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val		
	215					220					225						
acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	ggc	cac	tcc	ctg	atc	835	
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile		
	230				235					240				245			
gac	ggc	atc	aac	cgc	ggc	act	gac	atg	ctc	atg	ggc	ggc	aag	aac	gtg	883	
Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val		
			250					255					260				
ctt	gtc	tgc	ggg	tac	ggc	gat	gtc	ggc	aag	ggc	tgc	gct	gag	gct	ttc	931	
Leu	Val	Cys	Gly	Tyr	Gly	Asp	Val	Gly	Lys	Gly	Cys	Ala	Glu	Ala	Phe		

265	270	275	
gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac			979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn			
280	285	290	
gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag			1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu			
295	300	305	
gac atc gag gac gcc gac atc gtg atc acc ggc acc ggc aac aag gac			1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp			
310	315	320	325
atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg			1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu			
330	335	340	
ggc aac atc ggt tac ttt gat aat gag atc gat atg cat tcc ctg ttg			1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu			
345	350	355	
tac tgc gac gac gtc acc cgc acc aag atc aag cca cag atc gat gag			1219
His Arg Asp Asp Val Thr Arg Thr Ile Lys Pro Gln Val Asp Glu			
360	365	370	
atc acc ttc ttc aac ggt cgc tcc atc acc gtc ctg tcc aac ggt ggt			1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Gln Gly Arg			
375	380	385	
ctg ttc aac ctt ggt aac gcc acc gga cac cca tca ttc gtc atg tcc			1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser			
390	395	400	405
tac tct ttc gcc gat cag acc att ggc cag atc gaa ctg ttc caa aac			1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn			
410	415	420	
gaa gga cag tac gag aac gag gtc tac cgt ctg			1396
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu			
425	430		

0210 - 102

0211 - 432

0212 - PEST

0213 - *Corynebacterium glutamicum*

0400 - 102

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
 1 5 10 15

Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 30
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
 145 150 155 160
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
 165 170 175
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
 210 215 220
 Val Asp Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
 260 265 270
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
 275 280 285
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
 290 295 300
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys
 325 330 335
 Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp
 340 345 350
 Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys
 355 360 365
 Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
 370 375 380
 Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro

385

390

395

400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
420 425 430

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<211> 1358

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> 1(1)..(2385)

<223> RXN02085

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Met Thr Ser Asn Phe
1 5

tct tcc act gtc gtt gtt att cct cgc atc gga ggt aat cgt gaa ctg 165
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc gag ctg gaa ggt tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
25 30 35

ctt gca cag acc gcc cgc caa ttg gtc aac act gca tgg gat tct ttg 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
55 60 65

atg ctg gat acc gcc ggt att ttg ggt gtg ctg ccg gag cgt ttt gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
70 75 80 85

gac atc ggt gat cat gaa aac gat ggt ctg cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
90 95 100

tac ttt ggc ggt ggt cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctg gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
120 125 130

ggg gat aca cgt ttc gtt ttg gat ggc tcc ggc atg att gag gat ctg 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat ggc cgc cct gtt ctg gtt ggt Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly 150 155 160 165	595
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro 170 175 180	643
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctg atc aag Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys 185 190 195	691
tct ttc gat act gag tgg gtt cag atc gat gat cct gag ttg gtc acc Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr 200 205 210	739
gat att gct cct gag gtt ttg gag cca gtc cgc gct gat tac acc act Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr 215 220 225	787
ttg gat aag cgc gat gac ctg ttt gtc aat act tac ttc ggc tct ggc Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly 230 235 240 245	835
gat cag gat ctg aac act ctt gag ggc att cgc ttt gag gag att ggc Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly 250 255 260	883
gtn gac ttg gtc acc cat ggc gtc act gag ctt gct gag tgg aag ggt Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly 265 270 275	931
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cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
390 395 400 405	
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Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	
tcc acc act tgg gag cag tac gaa gag gca atg cgc gaa gaa atc gat	1459
Ser Ile Thr Leu Glu Gln Tyr Glu Gln Ala Met Arg Glu Gln Ile Asp	
440 445 450	
ctg ggc acc ggc aag cag gaa gaa ctt ggt ctt gat gtg ctg gtc ttc	1507
Leu Val Ile Ala Lys Gln Gln Glu Leu Gly Leu Asp Val Leu Val His	
455 460 465	
ggt gaa cca gag cgc aac gac aag gtt cag tac ttc tct gaa ctg ttc	1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Gln Leu Leu	
470 475 480 485	
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Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser	
490 495 500	
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Arg Lys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala	
505 510 515	
cca atc act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag	1699
Pro Met Thr Val Lys Pro Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys	
520 525 530	
cac ttc aag gga atg ctg acc ggt cca gtc aac ttc ctt gaa tgg ttc	1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser	
535 540 545	
tcc cct cgc gat gat cag cgt cgt gct acc aac gct gac cag gtc gaa	1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala	
550 555 560 565	
ctg gca ctg cgc gat gaa att aac gat ctc atc cag gct ggc gct aag	1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys	
570 575 580	
atc acc cag gtg gat gag cct cgc att cgt gaa ctg ttg ccc cta cca	1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg	
585 590 595	
gac ctc gat aag cct gcc tac ctg cag tgg tcc ctg gac tcc ttc cgc	1939
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg	
600 605 610	
ctg ggc act gcc ggc gca ccc gac gac gtc caa atc cac acc cag atg	1987
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met	
615 620 625	
tgc tac tcc gag ttc aac gaa gtg atc tcc tgg gtc atc ggc ttg gat	2035

Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
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 ggc gat gtc acc acc atc gaa gca gca ggt tcc gac atg cag gtc etc 2083
 Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
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 got ggt ctg aaa tct tcc gcc ttc gag etc gcc gtc gga cct ggt gtg 2131
 Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
 665 670 675
 tga gat atc cac tcc ccg cgg gtt cct tcc gag cag aaa gtg aac ggt 2179
 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
 680 685 690
 ctg etc gag ggt gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227
 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
 695 700 705
 aac cta gac tgt ggt cty aag acc ggt gga tgg cca gaa gtg gaa ggt 2275
 Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
 710 715 720 725
 tcc cta aag gtt etc gtt gag tcc ggt aag cag ggt cct gag aaa atc 2323
 Ser Leu Lys Val Leu Val Gln Ser Ala Lys Gln Ala Arg Glu Lys Ile
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<210> 104

<211> 749

<212> FRT

<213> Corynebacterium glutamicum

<400> 104

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 35 40 45
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445

Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
 580 585 590
 Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
 595 600 605
 Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
 610 615 620
 Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
 625 630 635 640
 Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
 645 650 655
 Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
 660 665 670
 Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
 675 680 685
 Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
 690 695 700
 Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
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 Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
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 740 745

<210> 105
 <211> 1923
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1900)

<223> FRXA02085

<400> 105

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Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
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aag ttc ggg ctg gaa ggc tac tgg aat gga tca att gaa ggt ttt gaa 211
Lys Phe Ala Leu Gln Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
25 30 35

ttt ggg caa acc ttt cgc caa ttg gtt aat act gaa tag gat ttt ttt 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
40 45 50

tct gga ttg gat tcc gtt cgc ttt gaa gga cgt tcc tac taa gaa gaa 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
55 60 65

atg ctg gat acc ggt gct att ttg ggt ttt ggt cgc gag cgt ttt gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
70 75 80 85

gac atc gct gat aat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg cgc gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
185 190 195

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tat ttc gat act gag tgg gtt cag atc gat gag cct gag ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gtt aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc cct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gta ctg aac act ctt gag ggc atc ggc att ggc gag att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
ggt gac tta gtc acc cat ggc gtc act gag cta gct gca tgg aag agt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
cag gag ctg ctg gtt cag ggc atc att gat ggt cct aat att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc tac tta tgt gct act ctt gct cct ctg cag cga tta gca gat cag	1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
305 310 315	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cca gtt cct tac	1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
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Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala	
330 335 340	
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Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu	
345 350 355	
gcc ggc aac atc gac ggc gct ggc ttc gat ggc gag tcc gca gca att	1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile	
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gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc	1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu	
375 380 385	
cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag	1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu	
390 395 400 405	
aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc	1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe	
410 415 420	
cca cag aac cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa	1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu	
425 430 435	

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
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 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485

gac ggt ttc ctc tca aac gac aac ggc tgg gtc caa agc tac ggc tcc 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca cgc 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530

cat gtc aac gga atg ctc acc ggt cca gtc acc atc att gca tgg tcc 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545

ttc gtt agt gat tat cag cag atg ggt acc acc ggt gac cca gtt gca 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565

ctg gaa ctg agc tat gaa att aac gat ctc atc gag tct gtt ggc aag 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580

atc atc cag gtg gat gag cct gag att cgt gaa ctg ttg ccc gct acc 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
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aga cgt cga taagcctgcc tacctgcagt ggt 1923
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<210> 106

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg

50	55	60
Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu 65 70 75 80		
Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro 85 90 95		
Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu 100 105 110		
Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu 115 120 125		
Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala 130 135 140		
Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg 145 150 155 160		
Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr 165 170 175		
Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr 180 185 190		
Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu 195 200 205		
Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg 210 215 220		
Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr 225 230 235 240		
Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly 245 250 255		
Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu 260 265 270		
Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly 275 280 285		
Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys 290 295 300		
Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu 305 310 315 320		
Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val 325 330 335		
Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu 340 345 350		
Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala 355 360 365		
Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro 370 375 380		

Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Gln Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Gln Leu Leu Asp Gly Ile Leu Ser Thr Ala Asn Gly Tyr Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Ile Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Tyr Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
 530 535 540
 Ile Leu Ala Tyr Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
 545 550 555 560
 Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
 565 570 575
 Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
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 Leu Leu Pro Ala Thr Arg Arg Arg
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<210> 107

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 107

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 Met Ser Leu Arg Phe

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gtg aac tgt tgc ccc cta cga gac gta gat aag cat gcc tac ctg cag 163
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Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
25 30 35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc 259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
40 45 50

tcc tgg gtc atc gag ttg gat gcc gat gtc acc acc atc gaa gca gaa 307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
55 60 65

agt tcc gac atg cag gtc ctc gcc gat gta ctg aac tcc tcc acc ttc gag 355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70 75 80 85

ctc ggc gtc gga cct ggt gtg tgg gat atc ctc tcc ccc cgc gtt cct 403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
90 95 100

tcc gcc cag aac gtg gac ggt ctc ctc gag gat gca ctg cag tcc gtc 451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
105 110 115

gat cat agc cag ctg tgg gtc aac cca gac tcc ggt ctg aag acc cat 499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
120 125 130

gga tgg cca gaa gtg gaa gct tcc cta aag gta ctc gtt aag tcc gct 547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
135 140 145

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aac 603

<210> 108

<211> 160

<212> FRT

<213> Corynebacterium glutamicum

<400> 108

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
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20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
50 55 60

Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
115 120 125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
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Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
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<210> 160

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> XXXXX2643

<400> 100

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Met Ser Gln Asn Arg
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atc agg acc aat cac gtt ggt tcc ttg ccc cgt acc caa gag ata att 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg agt tcc acc cct ggc aac atc gag ctg acc agc ttc ttt gat 451

Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp	
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Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser	
120 125 130	
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag tta acc gga	547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly	
135 140 145	
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Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu	
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Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala	
170 175 180	
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Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp	
185 190 195	
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa	739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu	
200 205 210	
taa aag atc atc att gat gaa ggt cta act gtt cag atc gac tta cgc	787
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro	
215 220 225	
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca aag ttg aag	835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys	
230 235 240 245	
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca	883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala	
250 255 260	
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc	931
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly	
265 270 275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att	979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile	
280 285 290	
ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca	1027
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala	
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Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu	
310 315 320 325	
ccf gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac	1123
Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn	
330 335 340	
gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc	1171
Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala	

345 350 355

aag ott gtt ggc cct gag aac gtc att ggc tcc act gac tgt ggt ctg 1219
 Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gga tgg gca gag ctg gag tcc cta 1267
 Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac 1313
 Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
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<210> 110

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320

Gln Glu Asn Lys Leu Pro Gln Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400

Phe

<210> 111
 <211> 548
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(525)
 <223> FRXA02648

<400> 111
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 Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15

agg gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat ggc atc 96
 Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

aac agt gca gtg aag ggc att cca aag gaa cag aac cgc ctg cac atc 144

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt 192
 Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

gac atc att gtt gag atc ctg cgc gca gag ttc ggt ggc ttc tcc ttc 240
 Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa 288
 Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

aac aag ctt cct gaa ggc tct gtt att tac cct ggt gtt atg tct cac 336
 Asn Lys Leu Pro Gln Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

tcc atc aac gtt gta gaa cac cca cgt ctg gtt gtt gat tct att gtt 384
 Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

cag ttc gcc aag ctt gtt ggc cct gag aac ttc att gag ttc act gag 432
 Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gaa aag ctt 480
 Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

gag tcc cta gta gag ggc gtt gtc att gca tca aag gaa ctg ttc 528
 Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

taagctagac aacgagggtt gct 576

<210> 112

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
 1 5 10 15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
165 170 175

<210> 113

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(784)

<223> PROACQUESE

<400> 113

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gagtttgata attttctttag acatttagat tggattttca atg agc cag aac agc 115
Met Ser Gln Asn Arg
1 5

atc agg acc act cac gtt ggt tcc ttg acc cgt acc cca gag cta gtt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc cag att ctg cac tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 461
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165

ctg aag aag ggc atg aac gca ggc gga gct aac gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195

att gat gaa gaa atg gtc gca gca tct gct gat ggt att tcc tgg gaa 749
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 114

<211> 328

<212> FRT

<213> Corynebacterium glutamicum

<100> 114

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn

130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

<210> 115
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC 1234

<400> 115
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 atettaacaa taatgtccat ataattttga aaagggtgaa gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5
 aac gag acc aac gcc acc aag gac gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20
 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35
 gcc ctg gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
 Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
 40 45 50
 tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
 Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
 55 60 65
 act ccg cag cca ggc gaa aag cca ctt tet att gct ctg cgt gag atc 355
 Thr Pro Gln Pro Gly Lys Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
 70 75 80 85
 aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct taaaacttca 405
 Asn Ala Gly Leu Leu Asp His Glu Glu Gly
 90 95

cac

408

1410 - 116

1411 - 35

1412 - PRT

1413 - Corynebacterium glutamicum

1400 - 116

Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
1 5 10 15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
20 25 30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
35 40 45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
50 55 60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
65 70 75 80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
85 90 95

1410 - 117

1411 - 1927

1412 - DNA

1413 - Corynebacterium glutamicum

1410

1411 - 208

1412 - (101)... (1804)

1413 - RX000128

1400 - 117

ccattttccg tttagttttg cctaaagaac ccgatggaaa ttatcgtgaa gcacccgatcc 60

cggttatccg tctagagaca ccgttggaag gggagcagca gtg agt aaa att tgg 115
Val Ser Lys Ile Ser
1 5

acg aaa cag aag gcc ctg acc gcg gtg ctg tct gtg acc act ccg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
10 15 20

gct ggg tgt tcc aag ctt ccg cag aac acg gat ccg caa gtg ctg ccg 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Gln Ile Ala Gly Pro Thr Pro
40 45 50

aat caa gat ccc gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
55 60 65

tat ccc aat cag cag tat gaa ggc ggc aag ggc tat ctg acg gaa ggg	355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly	
70 75 80 85	
acg cgc agc agc tgg aat ccc gct ggc tgc act cgt att ttg gat cgc	403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg	
90 95 100	
att gat ctg aac act ctg cca ggt tgc acg aat gag gaa cga acg att	451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile	
105 110 115	
ggc atc cgt gga acg cag gtc gga acg ttg ctg agc ggt ggc gtg tat	499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr	
120 125 130	
cag ccc tat aat ggc gag tta gaa cct gag atc agc atg cct cca gaa	547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu	
135 140 145	
gat ggg gat tgg cgt atc gat gat ttg cgc gat ggc att tta tta gag	595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu	
150 155 160 165	
aga aat gat ctg cgc aat gat gat act cgc gat gat atg gat tta tta	643
Arg Asn Arg Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Ile Phe	
170 175 180	
gat ccc tat ggc cag gtg ttg ctg ggc gat ccc cgt tgg ttg tta aat	691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn	
185 190 195	
gag tgc cag tgc atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt	739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly	
200 205 210	
cct tgc ccc gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat	787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp	
215 220 225	
ggc tgc ttc gtg ggc ttc aat gat ggc gag tat cag ttc act ggt ttg	835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu	
230 235 240 245	
gga aat ttg gat gat gat ggc cgt ttg cgt ttc gcc gcc cag gcc gtg	883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val	
250 255 260	
tgg acg ttg ggc cat gct gat gtc gca gcc ccc tac act ttg gtc gct	931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala	
265 270 275	
gac gcc ggc cgc ttg ctg tgc gag ttc cca acg ctg acc acc gat gac	979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp	
280 285 290	
ctc gac gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg	1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu	
295 300 305	

ttt gcg ttg cag gat gga tgg ttg tgg agg gtc agt tcc ggc aat gtg Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val 310 315 320 325	1075
agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca ggc Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala 330 335 340	1123
att tcc tcc tcc ggc aat gtg gtg gca ggc gta cgc aac gaa aac aac Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn 345 350 355	1171
gag gca gtg ctt act ggt ggc tcc atg gaa ggc gtg act tca gat ggc Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala 360 365 370	1219
ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac ggc tgg agt Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser 375 380 385	1267
ggg ttg tgg ggt ttg ggt gat ttg gag agt act gtc gga ttc gca tta Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg 390 395 400 405	1315
tcc gca gca aac ggt gag cta gtc cag acg gag ggc gag att gtg ttg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Gln Ile Val Leu 410 415 420	1363
cca agg gat gtg acg ggt ccc atc tct gaa ttc caa ctg tca cga act Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr 425 430 435	1411
ggc gtc ggc ggc ggc atg atc att gaa ggc agt gtg tac gtg ggc gtc Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val 440 445 450	1459
gta acg cgt cct ggt ccc ggc gag cgg cgc gtg aca aat atc acg gag Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu 455 460 465	1507
gtg ggc ccc agc ttg ggc gag ggc ggc ctg tgg atc aac tgg cgc cca Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro 470 475 480 485	1555
gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccc ctg tgg Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp 490 495 500	1603
cgc gtc gag cag gac gga tgg ggc att tgg tgg atg ccc agc ggc aat Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn 505 510 515	1651
ctc agc ggc ccc gtg gtc ggc gtg gca agt tcc ggc acg acg gtc tac Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr 520 525 530	1699
gtc act gat tgg cat ggc atg ctt cag ctg ccc act gcc gat aat gat Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp 535 540 545	1747
att tgg ggc gag gtg ccc ggt ttg ctg ggc acg cgt ggc ggc ccc gtg 550 555 560 565	1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc
Val Ala Tyr

1827

<210> 118

<211> 568

<212> FRT

<213> *Corynebacterium glutamicum*

<400> 118

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Ile Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Gln Ala Ala Lys Ala
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
210 215 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225 230 235 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
245 250 255

Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400
 Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
 405 410 415
 Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
 420 425 430
 Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
 435 440 445
 Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
 450 455 460
 Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
 465 470 475 480
 Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
 485 490 495
 Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
 500 505 510
 Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
 515 520 525
 Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
 530 535 540
 Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
 545 550 555 560
 Arg Ala Ala Pro Val Val Ala Tyr
 565

<210> 119
 <211> 1344
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1321)
 <223> RXA02240

<400> 119
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 Val Ala Gln Pro Thr
 1 5
 gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
 Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Gln Gly His Pro Asp
 10 15 20
 aaa ata ttt gat gct att ttt gat aat att ttg gtt ggt ctg ctg aaa 211
 Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
 25 30 35
 aaa gat cag cag tgg cgc gtc gca gtg gaa act gtt gtc acc acc gga 259
 Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly
 40 45 50
 atc gtc cat gtt gtt ttc aag gtc cgt acc agc gtt ttt gta gag atc 307
 Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile
 55 60 65
 cct caa tta gtc cgc aac aag ctg atc gaa atc gga ttc aac tcc tct 355
 Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser
 70 75 80 85
 gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt 403
 Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly
 90 95 100
 gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc 451
 Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala
 105 110 115
 cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac 499
 Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp
 120 125 130
 cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg 547
 Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met
 135 140 145
 cct ctg cct atc ggc ttg ggc cac cga ctg tca cgt cgt ctg acc cag 595
 Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln
 150 155 160 165
 gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc 643
 Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr
 170 175 180

cag gtc acc ttc gga tac gat gag caa gac agc cct agc cac atg gat	691
Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp	
185 190 195	
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg	739
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp	
200 205 210	
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Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp	
215 220 225	
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac	835
Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn	
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cct tca gtt ttt ttc att ctg ggt ggt cca atg ggt gat gca ggt ctg	853
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu	
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acc ggc cct aag atc atc gtg gat acc tac ggt agc atg gct agc cat	931
Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His	
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ggt ttt gaa gta ttt tcc gtt ggt gat tca gtc cca gta gac agc ttc	979
Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser	
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gct gca tac ggc atg cgt tgg gta gca aag aac atc gtg gca gca ggc	1027
Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly	
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ctt gct gat cgt gct gaa gtt cag gtt gca tac gca att gga agc gta	1075
Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala	
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aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc	1123
Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly	
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Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu	
345 350 355	
cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac	1219
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr	
360 365 370	
gct gac act gct gcc tac ggc cac ttt ggt agc act gat ttg gac ctt	1267
Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu	
375 380 385	
cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctg aag	1315
Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys	
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Leu Ala	

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<400> 120

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Asp	Ala	Leu	Leu	Gln	Lys	Asp	Pro	Gln	Ser	Arg	Val	Ala	Val	Glu	Thr
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Pro	Ser	His	Leu	Asp	Thr	Val	Val	Ile	Ser	Thr	Gln	His	Asp	Pro	Glu
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Val	Asp	Arg	Ala	Trp	Leu	Glu	Thr	Gln	Leu	Arg	Glu	His	Val	Ile	Asp
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Gly	Met	Ala	Arg	His	Gly	Gly	Gly	Ala	Phe	Ser	Gly	Lys	Asp	Pro	Ser
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Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn
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325 330 335

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340 345 350

Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu
355 360 365

Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg
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